

GenCore version 5.1.6
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Um protein - protein search, using sw mode.

Title: US-09-549-642-20
Perfect score: 138
Sequence: 1 IVGGXETTPHAYPQQVGLFIDDMYF 25
Scoring table: BLOSUM62
(Without arguments)
61.625 Million cell updates/sec

gapop 10.0 , gapext 0.3

ALIGNMENTS

RESULTS 1 S29239

chymotrypsin (EC 3.4.21.1) precursor - penaeid shrimp (*Penaeus vannamei*)

cdate: 22-Nov-1993 sequence_revision 26-May-1995 #text_change 22-Jun-1999
caccession: S29239 S22075

A ; title: Molecular Cloning Of A cDNA That Encodes A Serine Protease With Chymotrypsin-like Activity; A ; molecular number: S29239; MUID:92387359; PMID:1516690

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

הגדה הגדתית

Result No.	Score	Query Match	Length	DB ID	Description
1	101	73.2	271	2 S29239	chymotrypsin (EC 3.4.24.1)
2	94	68.1	265	2 T10495	chymotrypsin (EC 3.4.24.1)
3	91	65.9	31	2 S61558	chymotrypsin PM1
4	89	64.5	226	1 KCUF	brachytrypsin (EC 3.4.24.1)
5	80	58.0	31	2 S18356	chymotrypsin (EC 3.4.24.1)
6	74	53.6	309	2 B49878	coagulation factor
7	71	51.4	20	2 A56900	chymotrypsin I
8	69	50.0	271	2 A25528	pancreatic elastase
9	69	50.0	460	2 B61545	plasmin (EC 3.4.24.1)
10	69	50.0	1524	2 T30337	polyprotein - Af
11	68	49.3	25	2 A23698	tryptase (EC 3.4.24.1)
12	67	48.6	23	2 PU0036	serine proteinases
13	67	48.6	244	2 S72219	chymotrypsin B
14	67	48.6	268	2 S68826	pancreatic elastase
15	67	48.6	268	2 S68825	pancreatic elastase
16	66	47.8	271	1 ELRT2	granzyme A (EC 3.4.24.1)
17	65	47.1	262	1 A31372	pancreatic elastase
18	64	46.4	269	2 B26823	collagenolytic protein
19	63	45.7	20	2 A34817	pancreatic elastase
20	63	45.7	269	2 A26823	pancreatic elastase
21	63	45.7	273	2 A47246	tryptase (EC 3.4.24.1)
22	63	45.7	274	2 A45754	tryptase (EC 3.4.24.1)
23	63	45.7	275	2 C35863	tryptase (EC 3.4.24.1)
24	63	45.7	812	1 PLMS	plasmin (EC 3.4.24.1)
25	63	45.7	812	1 PLB30	plasmin (EC 3.4.24.1)
26	63	45.7	1420	2 A32869	apolipoprotein(a)
27	63	45.7	4548	1 S00657	apo(a)
28	62	44.9	24	2 PN0657	alkaline trypsin
			331	2 T27905	hypothetical protein

RESULT 1	S29339	Query N	RESULT 2	T10495
	chymotrypsin	Best Lc		chymotrypsin
	C;Species	Matched		C;Species
	C;Date: 2000-01-01			C;Date: 2000-01-01
	C;Access:			C;Access:
	R;Sellios			R;Sellios
	FEBS Lett			submitted
	A;Title:			A;Title:
	A;Referer:			A;Referer:
	A;Molecule:			A;Molecule:
	A;Residue:			A;Residue:
	A;Cross-refs:			A;Cross-refs:
	C;Superfamily:			C;Superfamily:
	C;Keywords:			C;Keywords:
	F;1-15/Dec-2000			F;1-15/Dec-2000
	F;16-27/Jan-2001			F;16-27/Jan-2001
	F;46-263			F;46-263
	F;86-132			F;86-132
QY	Db			

ALIGNMENTS

ALIGNMENTS

Query Match 68.1%; Score 94; DB 2; Length 265;
Best Local Similarity 68.0%; Pred. No. 8.6e-07;
Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0; Db

1 IVGGXEVTPHAYPWQVGLFIDDMYF 25

RESULT 5

S61538 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
chymotrypsin Pm1 - Penaeid shrimp (Penaeus monodon) (fragment)
C;Species: Penaeus monodon
C;Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 16-Feb-1997
C;Accession: S61558
R;Tsai, I.H.; Lu, P.J.; Chuang, J.L.
Biochim. Biophys. Acta 1080, 59-67, 1991
A;Title: The midgut chymotrypsins of shrimps (Penaeus monodon, Penaeus japonicus and Penaeus japonicus) and their homology with trypsin
A;Reference number: S61536; MUID:92031652; PMID:1657178
A;Accession: S61558
A;Molecule type: protein
A;Residues: 1-31 <TSA>
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase

Query Match 58.0%; Score 80; DB 2; Length 31;
Best Local Similarity 60.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 2; Mismatches 8; Indels 0; Gaps 0; Db

1 IVGGXEVTPHAYPWQVGLFIDDMYF 25

RESULT 6

B49878 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
coagulation factor G beta chain precursor - horseshoe crab (Tachypleus tridentatus)
C;Species: Tachypleus tridentatus
C;Date: 30-Jun-1995 #sequence_revision 30-Jun-1995 #text_change 20-Jun-2000
C;Accession: B49878
R;Seki, N.; Mutu, T.; Oda, T.; Iwaki, D.; Kuma, K.; Miyata, T.; Iwanaga, S.
J. Biol. Chem. 269, 1370-1374, 1994
A;Title: Horseshoe crab (1,3)-beta-D-glucan-sensitive coagulation factor G. A serine
A;Reference number: A49878; MUID:94117453; PMID:8288603
A;Accession: B49878
A;Molecule type: mRNA
A;Status: preliminary
A;Cross-references: GB:D16623; NID:9459415; PID:BA004045.1; PMID:9459416
C;Superfamily: trypsin; trypsin homology
C;Keywords: hemolymph coagulation; heterodimer; serine proteinase; zymogen
F;47-287/Domain: trypsin homology <TRY>

Query Match 53.6%; Score 74; DB 2; Length 309;
Best Local Similarity 57.9%; Pred. No. 0.0012; Mismatches 4; Indels 0; Gaps 0; Db

1 IVGGXEVTPHAYPWQVGLFIDDMYF 25

RESULT 7

A56900 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
chymotrypsin I (EC 3.4.21.1) - penaeid shrimp (Penaeus vanamei) (fragment)
C;Species: Penaeus vanamei
C;Accession: A56900
R;Van Wormhout, A.; Le Chevallier, P.; Sellos, D.
Comp. Biochem. Physiol. B 103, 675-680, 1992
A;Title: Purification, biochemical characterization and N-terminal sequence of a serine
apoda
A;Reference number: A56900; MUID:93092601; PMID:1458841
A;Accession: A56900

Query Match 64.5%; Score 89; DB 1; Length 226;
Best Local Similarity 64.0%; Pred. No. 4.2e-06;
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0; Db

1 IVGGXEVTPHAYPWQVGLFIDDMYF 25

Q: Note: sequence extracted from NCBI backbone (NCBIP:120229)

A;Note: a second variant, designated chymotrypsin II, had an identical N-terminal sequence.
C;Comment: this enzyme has chymotryptic and collagenolytic activities.
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase
Query Match 51.4%; Score 71; DB 2; Length 20;
Best Local Similarity 65.0%; Pred. No. 0.00016;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 1 IVGGXEVTPHAYPQVQGLFI 20
Db 1 IVGGXEVTPHAYPQVQGLFI 20
RESULT 8
A25528 pancreatic elastase II (EC 3.4.21.71) precursor - mouse
C;Species: <i>Mus musculus</i> (house mouse)
C;Date: 30-Jun-1998 #sequence_revision 30-Jun-1998 #text_change 22-Jun-1999
A;Accession: A25528
A;Title: Sequence organisation and transcriptional regulation of the mouse elastase II a
A;Reference number: A93646; MUID:87066713; PMID:3041189
A;Accession: A25528
A;Molecule type: mRNA
A;Residues: 1-271 <STE>
A;Cross-references: GB:X04573; NID:950825; PIDN:CAA28242.1; PID:950826
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F1:1-30/Domain: signal sequence #status predicted <SIG>
F1:1-271/Domain: pancreatic elastase II #status predicted <MAT>
F1:1-264/Domain: trypsin homology <TRY>
F1:75,123,218/Active site: His, Asp, Ser #status predicted
Query Match 50.0%; Score 69; DB 2; Length 271;
Best Local Similarity 61.1%; Pred. No. 0.006;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 IVGGXEVTPHAYPQVQGL 18
Db 1 IVGGXEVTPHAYPQVQGL 18
RESULT 9
B61545 plasmin (EC 3.4.21.7) precursor - sheep (fragments)
N;Alternative names: plasminogen
N;Keywords: miniplasminogen
C;Species: <i>Ovis ammon aries</i> (domestic sheep)
C;Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 17-Mar-1999
C;Accession: B61545; S28200
R;Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
A;Title: Structural aspects of the plasminogen of various species.
A;Reference number: A61545; MUID:89005015; PMID:3168975
A;Accession: B61545
A;Molecule type: protein
A;Residues: 1-37-38-117 <SCH>
R;Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.
Protein Seq. Data Anal. 5, 21-25, 1992
A;Title: Complete amino acid sequence of ovine miniplasminogen.
A;Reference number: S28200; MUID:93149995; PMID:1492092
A;Accession: S28200
A;Molecule type: protein
A;Residues: 118-460 <SCC>
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase; z
F1:1-37-38-117-118-460/Product: plasminogen (fragments) #status experimental <PRO>
F1:1-37/Domain: activation peptide (fragment) #status experimental <APT>
F1:38-117-118-230-241-460/Product: plasmin (fragments) #status experimental <MAT>
F1:41-118/Domain: kringle homology #status experimental <KR>
F1:18-46/Domain: miniplasminogen #status experimental <MIN>

Result No.	Score	Query Match	Length	DB ID	Description
1	136	98.6	25	5 US-09-303-375A-1	Sequence 1, Appli
2	136	98.6	25	5 US-09-303-375A-2	Sequence 2, Appli
3	136	98.6	25	5 US-09-303-375A-3	Sequence 1, Appli
4	136	98.6	25	5 US-09-303-375A-4	Sequence 2, Appli
5	136	98.6	25	5 US-09-303-375A-5	Sequence 1, Appli
6	136	98.6	300	5 US-09-303-375A-6	Sequence 2, Appli
7	101	73.2	25	5 US-09-303-375A-7	Sequence 1, Appli
8	101	73.2	25	5 US-09-303-375A-8	Sequence 2, Appli
9	101	73.2	25	5 US-09-303-375A-9	Sequence 3, Appli
10	91	65.9	25	5 US-09-303-375A-10	Sequence 4, Appli
11	91	65.9	25	5 US-09-303-375A-11	Sequence 5, Appli
12	91	65.9	25	5 US-09-303-375A-12	Sequence 6, Appli
13	89	64.5	25	5 US-09-303-375A-13	Sequence 7, Appli
14	89	64.5	25	5 US-09-303-375A-14	Sequence 8, Appli
15	89	64.5	25	5 US-09-303-375A-15	Sequence 9, Appli
16	80	58.0	25	5 US-09-303-375A-16	Sequence 10, Appli
17	80	58.0	25	5 US-09-303-375A-17	Sequence 11, Appli
18	80	58.0	25	5 US-09-303-375A-18	Sequence 12, Appli
19	75.5	54.7	287	1 PCT-US02-10780-130	Sequence 13, Appli
20	75.5	54.7	287	6 US-10-114-270-130	Sequence 14, Appli
21	75.5	54.7	602	7 US-60-452-680-233-38	Sequence 15, Appli
22	75.5	54.7	922	1 PCT-US02-10366-52	Sequence 16, Appli
23	75.5	54.7	932	6 US-10-163-937-6	Sequence 17, Appli
24	75.5	54.7	986	1 PCT-US02-10166-50	Sequence 18, Appli
25	70	50.7	273	6 US-10-219-051B-8824	Sequence 19, Appli
26	70	50.7	273	6 US-10-219-051B-13255	Sequence 20, Appli

NUMBER OF SEQ ID NOS: 20
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 25
 TYPE: PRT
 ORGANISM: Euphausia superba
 US-09-303-375A-2

Query Match 98.6%; Score 136; DB 5; Length 25;
 Best Local Similarity 96.0%; Pred. No. 1.4e-13; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 SEQ ID NO 2
 LENGTH: 25
 TYPE: PRT
 ORGANISM: Euphausia superba
 US-09-549-642-2

Query Match 98.6%; Score 136; DB 5; Length 25;
 Best Local Similarity 96.0%; Pred. No. 1.4e-13; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 SEQ ID NO 2
 LENGTH: 25
 TYPE: PRT
 ORGANISM: Euphausia superba
 US-09-549-642-2

RESULT 3
 US-09-549-642-1
 Sequence 1, Application US/09549642
 GENERAL INFORMATION:
 APPLICANT: Phairson Medical, Inc.
 APPLICANT: de Faire, Johan
 APPLICANT: Franklin, Richard L.
 APPLICANT: Lindblom, Ragnvald
 TITLE OF INVENTION: Removing Dental Plaque with Krill
 FILE REFERENCE: 314572-101F
 CURRENT APPLICATION NUMBER: US/09/549, 642
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 09/303, 375
 PRIOR FILING DATE: 2000-04-30
 PRIOR APPLICATION NUMBER: 08/600, 273
 PRIOR FILING DATE: 1996-02-08
 PRIOR APPLICATION NUMBER: 08/486, 820
 PRIOR FILING DATE: 1995-06-07
 PRIOR APPLICATION NUMBER: 08/385, 540
 PRIOR FILING DATE: 1995-02-08
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 25
 TYPE: PRT
 ORGANISM: Euphausia superba
 US-09-549-642-1

Query Match 98.6%; Score 136; DB 5; Length 25;
 Best Local Similarity 96.0%; Pred. No. 1.4e-13; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 SEQ ID NO 1
 LENGTH: 25
 TYPE: PRT
 ORGANISM: Euphausia superba
 US-09-549-642-1

RESULT 4
 US-09-549-642-2
 Sequence 2, Application US/09549642
 GENERAL INFORMATION:
 APPLICANT: Phairson Medical, Inc.
 APPLICANT: de Faire, Johan
 APPLICANT: Franklin, Richard L.
 APPLICANT: Lindblom, Ragnvald
 APPLICANT: Kay, John
 TITLE OF INVENTION: Removing Dental Plaque with Krill
 FILE REFERENCE: 314572-101F
 CURRENT APPLICATION NUMBER: US/09/549, 642
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 09/303, 375
 PRIOR FILING DATE: 2000-04-30
 PRIOR APPLICATION NUMBER: 08/600, 273
 PRIOR FILING DATE: 1996-02-08
 PRIOR APPLICATION NUMBER: 08/486, 820
 PRIOR FILING DATE: 1995-06-07
 PRIOR APPLICATION NUMBER: 08/385, 540
 PRIOR FILING DATE: 1995-02-08
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 25
 TYPE: PRT
 ORGANISM: Euphausia superba
 US-09-549-642-2

RESULT 5
 US-09-549-642-20
 Sequence 20, Application US/09549642
 GENERAL INFORMATION:
 APPLICANT: Phairson Medical, Inc.
 APPLICANT: de Faire, Johan
 APPLICANT: Franklin, Richard L.
 APPLICANT: Lindblom, Ragnvald
 APPLICANT: Kay, John
 TITLE OF INVENTION: Removing Dental Plaque with Krill
 FILE REFERENCE: 314572-101F
 CURRENT APPLICATION NUMBER: US/09/549, 642
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 09/303, 375
 PRIOR FILING DATE: 2000-04-30
 PRIOR APPLICATION NUMBER: 08/600, 273
 PRIOR FILING DATE: 1996-02-08
 PRIOR APPLICATION NUMBER: 08/486, 820
 PRIOR FILING DATE: 1995-06-07
 PRIOR APPLICATION NUMBER: 08/385, 540
 PRIOR FILING DATE: 1995-02-08
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 20
 LENGTH: 25
 TYPE: PRT
 ORGANISM: Euphausia superba
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (1) .. (25)
 OTHER INFORMATION: Xaa = Any Amino Acid
 US-09-549-642-20

RESULT 6
 US-09-644-022A-1
 Sequence 1, Application US/09644022A
 GENERAL INFORMATION:
 APPLICANT: Franklin, Richard L.
 APPLICANT: Cowling, Didier S.P.
 APPLICANT: Hubbel, Jeffrey A.
 APPLICANT: van de Wetering, Petra

TITLE OF INVENTION: Treatment of Trauma
 FILE REFERENCE: 314572-103B
 CURRENT APPLICATION NUMBER: US/09/644,022A
 CURRENT FILING DATE: 2000-08-23
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 300
 TYPE: PRT
 ORGANISM: Panaeus vanameii
 US-09-644-022A-1

Query Match 73.2%; Score 101; DB 5; Length 25;
 Best Local Similarity 72.0%; Pred. No. 2.9e-08;
 Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPMQVGLFIDDMYF 25
 Db 1 IVGGXEVTPHAYPMQVGLFIDDMYF 25

RESULT 9
 US-09-549-642-3

Sequence 3, Application US/09549642
 GENERAL INFORMATION:
 APPLICANT: Phairson Medical, Inc.
 APPLICANT: de Faire, Johan
 APPLICANT: Franklin, Richard L.
 APPLICANT: Kay, John
 APPLICANT: Lindblom, Ragnvald
 TITLE OF INVENTION: Removing Dental Plaque with Krill
 TITLE OF INVENTION: Enzymes
 FILE REFERENCE: 314572-101F
 CURRENT APPLICATION NUMBER: US/09/549,642
 CURRENT FILING DATE: 2000-04-14
 PRIORITY APPLICATION NUMBER: 09/303,375
 PRIORITY APPLICATION NUMBER: 2000-04-30
 PRIORITY APPLICATION NUMBER: 08/600,273
 PRIORITY APPLICATION NUMBER: 1996-02-08
 PRIORITY APPLICATION NUMBER: 08/486,820
 PRIORITY APPLICATION NUMBER: 1995-06-07
 PRIORITY APPLICATION NUMBER: 08/385,540
 PRIORITY APPLICATION NUMBER: 1995-02-08
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 25
 TYPE: PRT
 ORGANISM: Panaeus vanameii
 US-09-549-642-3

Query Match 73.2%; Score 101; DB 5; Length 25;
 Best Local Similarity 72.0%; Pred. No. 2.9e-08;
 Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPMQVGLFIDDMYF 25
 Db 1 IVGGXEVTPHAYPMQVGLFIDDMYF 25

RESULT 10
 US-09-644-022A-6

Sequence 6, Application US/09644022A
 GENERAL INFORMATION:
 APPLICANT: Franklin, Richard L.
 APPLICANT: Cowling, Didier S.P.
 APPLICANT: Hubel, Jeffrey A.
 APPLICANT: van de Wetering, Petra
 TITLE OF INVENTION: Treatment of Trauma
 FILE REFERENCE: 314572-103B
 CURRENT APPLICATION NUMBER: US/09/644,022A
 CURRENT FILING DATE: 2000-08-23
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 6
 LENGTH: 25
 TYPE: PRT
 ORGANISM: Panaeus monodon chymotryptic
 US-09-644-022A-6

Query Match 65.9%; Score 91; DB 5; Length 25;
 Best Local Similarity 64.0%; Pred. No. 9.7e-07;
 Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPMQVGLFIDDMYF 25
 Db 1 IVGGXEVTPHAYPMQVGLFIDDMYF 25

Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
 Db 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25

RESULT 11
 US-09-303-375A-7
 ; Sequence 7, Application US/09303375A
 ; GENERAL INFORMATION:
 ; APPLICANT: Johan R. de Faire
 ; APPLICANT: Richard L. Franklin
 ; APPLICANT: John Kay
 ; APPLICANT: Ragnvald Lindblom
 ; TITLE OF INVENTION: Multifunctional Enzyme
 ; FILE REFERENCE: 314572-101E
 ; CURRENT APPLICATION NUMBER: US/09/303,375A
 ; CURRENT FILING DATE: 1999-04-30
 ; PRIORITY APPLICATION NUMBER: US 08/486,820
 ; PRIORITY FILING DATE: 1995-06-07
 ; PRIORITY APPLICATION NUMBER: US 08/385,540
 ; PRIORITY FILING DATE: 1995-02-08
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: *Penaeus monodon*
 US-09-303-375A-7

Query Match 65.9%; Score 91; DB 5; Length 25;
 Best Local Similarity 64.0%; Pred. No. 9.7e-07;
 Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
 Db 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25

RESULT 12
 US-09-549-642-7
 ; Sequence 7, Application US/09549642
 ; GENERAL INFORMATION:
 ; APPLICANT: Phairson Medical, Inc.
 ; APPLICANT: de Faire, Johan
 ; APPLICANT: Franklin, Richard L.
 ; APPLICANT: Kay, John
 ; APPLICANT: Lindblom, Ragnvald
 ; TITLE OF INVENTION: Removing Dental Plaque with Kriil
 ; TITLE OF INVENTION: Enzymes
 ; FILE REFERENCE: 314572-101F
 ; CURRENT APPLICATION NUMBER: US/09/549,642
 ; PRIORITY FILING DATE: 2000-04-14
 ; PRIORITY APPLICATION NUMBER: 09/303,375
 ; PRIORITY FILING DATE: 2000-04-30
 ; PRIORITY APPLICATION NUMBER: 08/600,273
 ; PRIORITY FILING DATE: 1996-02-08
 ; PRIORITY APPLICATION NUMBER: 08/486,820
 ; PRIORITY FILING DATE: 1995-06-07
 ; PRIORITY APPLICATION NUMBER: 08/385,540
 ; PRIORITY FILING DATE: 1995-02-08
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: *Penaeus monodon*
 US-09-549-642-7

Query Match 65.9%; Score 91; DB 5; Length 25;
 Best Local Similarity 64.0%; Pred. No. 9.7e-07;
 Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
 Db 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25

RESULT 13
 US-09-644-022A-7
 ; Sequence 7, Application US/09644022A
 ; GENERAL INFORMATION:
 ; APPLICANT: Franklin, Richard L.
 ; APPLICANT: Cowling, Didier S.P.
 ; APPLICANT: Hubbel, Jeffrey A.
 ; APPLICANT: van de Watering, Petra
 ; TITLE OF INVENTION: Treatment of Trauma
 ; FILE REFERENCE: 314572-103B
 ; CURRENT APPLICATION NUMBER: US/09/644,022A
 ; CURRENT FILING DATE: 2000-08-23
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: *Uca pugilator* enzyme
 US-09-644-022A-7

Query Match 64.5%; Score 89; DB 5; Length 25;
 Best Local Similarity 64.0%; Pred. No. 2e-06;
 Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
 Db 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25

RESULT 14
 US-09-303-375A-8
 ; Sequence 8, Application US/09303375A
 ; GENERAL INFORMATION:
 ; APPLICANT: Johan R. de Faire
 ; APPLICANT: Richard L. Franklin
 ; APPLICANT: John Kay
 ; APPLICANT: Ragnvald Lindblom
 ; TITLE OF INVENTION: Multifunctional Enzyme
 ; FILE REFERENCE: 314572-101E
 ; CURRENT APPLICATION NUMBER: US/09/303,375A
 ; CURRENT FILING DATE: 1999-04-30
 ; PRIORITY APPLICATION NUMBER: US 08/486,820
 ; PRIORITY FILING DATE: 1995-06-07
 ; PRIORITY APPLICATION NUMBER: US 08/385,540
 ; PRIORITY FILING DATE: 1995-02-08
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: *Uca pugilator*
 US-09-303-375A-8

Query Match 64.5%; Score 89; DB 5; Length 25;
 Best Local Similarity 64.0%; Pred. No. 2e-06;
 Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
 Db 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25

RESULT 15
 US-09-549-642-8
 ; Sequence 8, Application US/09549642
 ; GENERAL INFORMATION:
 ; APPLICANT: Phairson Medical, Inc.
 ; APPLICANT: de Faire, Johan
 ; APPLICANT: Franklin, Richard L.

Query Match 65.9%; Score 91; DB 5; Length 25;
 Best Local Similarity 64.0%; Pred. No. 9.7e-07;
 Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25

APPLICANT: Kay, John
APPLICANT: Lindblom, Ragnvald
TITLE OF INVENTION: Removing Dental Plaque with Krill
TITLE OF INVENTION: Enzymes
FILE REFERENCE: 314572-101F
CURRENT APPLICATION NUMBER: US/09/549,642
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 09/303,375
PRIOR FILING DATE: 2000-04-30
PRIOR APPLICATION NUMBER: 08/600,273
PRIOR FILING DATE: 1996-02-08
PRIOR APPLICATION NUMBER: 08/486,820
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/385,540
PRIOR FILING DATE: 1995-02-08
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 25
TYPE: PRT
ORGANISM: Uca pugilator
9-549-642-8

Search completed: May 30, 2003, 11:12:20
Search time: 89 secs

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GenCore version 5.1.6
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DM protein - protein search, using SW model

Run on: May 30, 2003, 11:01:13 ; Search time 26 Seconds
(without alignments)
28.291 Million cell updates/sec

Title: US-09-549-642-20
Perfect score: 138
Sequence: 1 IVGEXEVTPHAYPMQVGLFTDDMYF 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 2942922 residues
number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:
5: /cgn2_6/ptodata/1/1aa/PECTUS_COMB.pep:
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-08-385-540A-1
Sequence 1, Application US/08385540A
; Patient No. 5945102
; GENERAL INFORMATION:
; APPLICANT: de Faire, Johan
; TITLE OF INVENTION: Wound Care With Multifunctional
; TITLE OF INVENTION: Enzyme
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSEQ for Windows version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,540A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/600,273
; FILING DATE: 01-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 314572-101A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609 520-214
; TELEFAX: 609 520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-385-540A-1

SEQUENCE MATCHES

Result No.	Score	Query Match	Length	DB ID	Description
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2	136	98.6	25	2 US-08-385-540A-1	Sequence 2, Appli
3	136	98.6	25	2 US-08-385-540A-17	Sequence 17, Appli
4	136	98.6	25	2 US-08-600-273A-1	Sequence 1, Appli
5	136	98.6	25	2 US-08-600-273A-2	Sequence 2, Appli
6	136	98.6	25	2 US-08-600-273A-17	Sequence 17, Appli
7	136	98.6	25	3 US-08-486-820-1	Sequence 1, Appli
8	136	98.6	25	3 US-08-486-820-2	Sequence 2, Appli
9	136	98.6	25	3 US-08-486-820-17	Sequence 17, Appli
10	136	98.6	25	3 US-08-705-875A-19	Sequence 19, Appli
11	136	98.6	25	4 US-09-220-731-1	Sequence 1, Appli
12	136	98.6	25	4 US-09-220-731-2	Sequence 2, Appli
13	136	98.6	25	4 US-09-220-731-20	Sequence 20, Appli
14	136	98.6	25	4 US-09-220-731-20	Sequence 8, Appli
15	136	98.6	25	4 US-09-220-731-23	Sequence 10, Appli
16	136	98.6	25	4 US-09-220-731-19	Sequence 23, Appli
17	136	98.6	300	3 US-08-705-875A-4	Sequence 24, Appli
18	136.	98.6	300	3 US-08-705-875A-6	Sequence 4, Appli
19	136	98.6	300	4 US-09-220-731-21	Sequence 6, Appli
20	136	98.6	302	4 US-09-220-731-26	Sequence 21, Appli
21	136	98.6	308	4 US-09-705-875A-8	Sequence 26, Appli
22	123	89.1	23	4 US-09-220-731-23	Sequence 10, Appli
23	101	73.2	25	2 US-08-540A-3	Sequence 19, Appli
24	101	73.2	25	3 US-08-600-273A-1	Sequence 3, Appli
25	101	73.2	25	3 US-08-486-820-3	Sequence 3, Appli
26	101	73.2	25	4 US-09-220-731-31	Sequence 25, Appli
27	96	69.6	211	4 US-09-220-731-25	Sequence 25, Appli

Query Match Best Local Similarity 98.6%; Score 136; DB 2; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Qy 1 IVGGEVPHAYPMQVGLFTDDYF

1 IVCGSNEVTPHAYPWOVGLIEIDDMYF 25

TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-620-2124
TELEFAX: 609-620-3259
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
J5-08-600-273A-1

Query Match 98.6%; S
Best Local Similarity 96.0%; P
Matches 24; Conservative 0;

1 IVGGXEVTPHAYPHQVQVGLFD
1 IVGGXEVTPHAYPHQVQVGLFD

Py
Ddb
RT 5
J5-08-600-273A-2
; Sequence 2, Application US/086002
Patent No. 5984806
GENERAL INFORMATION:
APPLICANT: de Faire, Johan
APPLICANT: Franklin, Richard
APPLICANT: Kay, John
TITLE OF INVENTION: Acne Treata
TITLE OF INVENTION: Enzyme Treata
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Decher Price &
STREET: 997 Lenox Drive, Bu
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 9
SOFTWARE: FASTSEQ for Windo
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/6
FILING DATE: 08-FEB-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/395,
FILING DATE: 08-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29-135
REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-620-2124
TELEFAX: 609-620-3259
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
J5-08-600-273A-2

Query Match 98.6%; S
Best Local Similarity 96.0%; P
Matches 24; Conservative 0;

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RESULT 6
US-08-600-273A-17
; Sequence 17, Application US/08600273A
; Patent No. 5958406
; GENERAL INFORMATION:
; APPLICANT: de Faire, Johan L.
; APPLICANT: Franklin, Richard L.
; TITLE OF INVENTION: Acne Treatment With Multifunctional
; TITLE OF INVENTION: Enzyme
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600, 273A
; FILING DATE: 08-FEB-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486, 820
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/385, 540
; FILING DATE: 08-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 314572-101C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-620-3214
; TELEFAX: 609-620-3214
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-600-273A-17

Query Match 98.6%; Score 136; DB 2; Length 2
; Best Local Similarity 100.0%; Pred. No. 3.5e-15;
; Matches 25; Conservative 0; Mismatches 0; Indels 0
; APPLICANT: de Faire, Johan L.
; APPLICANT: Franklin, Richard L.
; APPLICANT: Kay, John
; TITLE OF INVENTION: Antimicrobial Uses Of Multifunctional

RESULT 7
US-08-486-820-1
; Sequence 1, Application US/08486820
; Patent No. 6030612
; GENERAL INFORMATION:
; APPLICANT: de Faire, Johan L.
; APPLICANT: Franklin, Richard L.
; APPLICANT: Kay, John
; TITLE OF INVENTION: Antimicrobial Uses Of Multifunctional

```

TITLE OF INVENTION: Enzyme
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dechert Price & Rhoads
 STREET: 997 Lenox Drive, Building 3, Suite 210
 CITY: Lawrenceville
 STATE: NJ
 ZIP: 08543
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSEQ for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/486,820
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/486,820
 FILING DATE: 07-JUNE-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: BLOOM, Allen
 REGISTRATION NUMBER: 29,135
 REFERENCE/DOCKET NUMBER: 314572-101B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 609-620-3214
 TELEFAX: 609-620-3259
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-486-820-1

Query Match 98.6%; Score 136; DB 3; Length 25;
 Best Local Similarity 96.0%; Pred. No. 3.5e-15; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWNQVGLFDDMF 25
 Db 1 IVGGNEVTPHAYPWNQVGLFDDMF 25

RESULT 8
 US-08-486-820-2
 Sequence 2, Application US/08486820
 Patent No: 6030612
 GENERAL INFORMATION:
 APPLICANT: de Faire, Johan
 APPLICANT: Franklin, Richard L.
 TITLE OF INVENTION: Enzyme
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dechert Price & Rhoads
 STREET: 997 Lenox Drive, Building 3, Suite 210
 CITY: Lawrenceville
 STATE: NJ
 COUNTRY: USA
 ZIP: 08543
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSEQ for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/486,820
 FILING DATE: 07-JUNE-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: BLOOM, Allen
 REGISTRATION NUMBER: 29,135
 REFERENCE/DOCKET NUMBER: 314572-101B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 609-620-3214
 TELEFAX: 609-620-3259
 TELEX:
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-486-820-17

Query Match 98.6%; Score 136; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.e-15; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVGGXEVTHAYPHQVGLFIDDMYF 25
 Db 1 IVGGXEVTHAYPHQVGLFIDDMYF 25

RESULT 10
 US-08-705-875A-19
 ; Sequence 19, Application US/08705875A
 ; Patent No. 604015
 ; GENERAL INFORMATION:
 ; APPLICANT: Kille, Peter
 ; TITLE OF INVENTION: ENZYME AND DNA SEQUENCE ENCODING
 ; TITLE OF INVENTION: SAME
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; STREET: Decher Price & Rhoads
 ; CITY: Lawrenceville
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08543
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: FastSEQ for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/04/705,875A
 ; FILING DATE: 28-AUG-1996
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/768,318
 ; FILING DATE: 17-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bloom, Allen
 ; REGISTRATION NUMBER: 29,135
 ; REFERENCE/DOCKET NUMBER: 314572-102US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 609-520-3214
 ; TELEFAX: 609-520-3259
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25 amino acids
 ; TYPE: amino acid
 ; STRANGENESS: Single
 ; TOPOLOGY: Linear
 ; US-08-705-875A-19

Query Match 98.6%; Score 136; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.e-15; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVGGXEVTHAYPHQVGLFIDDMYF 25
 Db 1 IVGGXEVTHAYPHQVGLFIDDMYF 25

RESULT 11
 US-09-220-731-1
 ; Sequence 1, Application US/09220731A
 ; Patent No. 6232088
 ; GENERAL INFORMATION:
 ; APPLICANT: Phairson Medical, Inc.
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Yves St. Pierre
 ; TITLE OF INVENTION: Treatment and Prevention of Immune

; FILE REFERENCE: 314572-101D
 ; CURRENT APPLICATION NUMBER: US/09/220731A
 ; FILING DATE: 1998-12-24
 ; EARLIER APPLICATION NUMBER: PCT/SE93/00455
 ; EARLIER FILING DATE: 1993-05-21
 ; EARLIER APPLICATION NUMBER: 08/338,501
 ; EARLIER FILING DATE: 1994-11-22
 ; EARLIER APPLICATION NUMBER: 08/385,540
 ; EARLIER FILING DATE: 1995-02-08
 ; EARLIER APPLICATION NUMBER: 08/486,820
 ; EARLIER FILING DATE: 1995-06-07
 ; EARLIER APPLICATION NUMBER: 08/600,273
 ; EARLIER FILING DATE: 1996-02-08
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: Euphasia superba
 ; US-09-220-731-1

Query Match 98.6%; Score 136; DB 4; Length 25;
 Best Local Similarity 96.0%; Pred. No. 3.e-15; Indels 1; Gaps 0;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVGGXEVTHAYPHQVGLFIDDMYF 25
 Db 1 IVGGXEVTHAYPHQVGLFIDDMYF 25

Query Match 98.6%; Score 136; DB 4; Length 25;
 Best Local Similarity 96.0%; Pred. No. 3.e-15; Indels 0; Gaps 0;

Qy 1 IVGGXEVTHAYPHQVGLFIDDMYF 25
 Db 1 IVGGXEVTHAYPHQVGLFIDDMYF 25

RESULT 13
 US-09-220-731-20

Sequence 20, Application US/09220731A
 GENERAL INFORMATION
 APPLICANT: Phairson Medical, Inc.
 APPLICANT: Richard L. Franklin
 APPLICANT: Yves St. Pierre
 TITLE OF INVENTION: Treatment and Prevention of Immune Rejection Reactions
 FILE REFERENCE: 314572-101D
 CURRENT APPLICATION NUMBER: US/09/220,731A
 CURRENT FILING DATE: 1998-12-24
 EARLIER APPLICATION NUMBER: PCT/SE93/00455
 EARLIER FILING DATE: 1993-05-21
 EARLIER APPLICATION NUMBER: 08/338,501
 EARLIER FILING DATE: 1994-11-22
 EARLIER APPLICATION NUMBER: 08/385,540
 EARLIER FILING DATE: 1995-02-08
 EARLIER APPLICATION NUMBER: 08/486,820
 EARLIER FILING DATE: 1995-06-07
 EARLIER APPLICATION NUMBER: 08/600,273
 EARLIER FILING DATE: 1996-02-08
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 20
 LENGTH: 25
 TYPE: PRT
 ORGANISM: Euphasia superba
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (5)...(5)
 OTHER INFORMATION: xaa = Any Amino Acid
 US-09-220-731-20

Query Match 98.6%; Score 136; DB 4; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.5e-15;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPQVQGLFIDDMYF 25
 Db 1 IVGGXEVTPHAYPQVQGLFIDDMYF 25

RESULT 14
 US-08-705-875A-8
 Sequence 8, Application US/08705875A
 GENERAL INFORMATION:
 APPLICANT: Key, John
 APPLICANT: Kille, Peter
 TITLE OF INVENTION: ENZYME AND DNA SEQUENCE ENCODING
 TITLE OF INVENTION: SAME
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Dechert Price & Rhoads
 STREET: 997 Lenox Drive, Building 3, Suite 210
 CITY: Lawrenceville
 STATE: NJ
 ZIP: 08543
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: PasteSEQ for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/705,875A
 CLASSIFICATION: 514
 FILING DATE: 28-AUG-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/768,318
 FILING DATE: 17-DEC-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Bloom, Allen

REGISTRATION NUMBER: 29,135
 REFERENCE/DOCKET NUMBER: 314572-102US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 609-520-3214
 TELEX: 609-520-3259
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 178 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-705-875A-8

Query Match 98.6%; Score 136; DB 3; Length 178;
 Best Local Similarity 96.0%; Pred. No. 3.3e-14;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPQVQGLFIDDMYF 25
 Db 72 IVGGXEVTPHAYPQVQGLFIDDMYF 96

RESULT 15
 US-09-220-731-23
 Sequence 23, Application US/09220731A
 Patent No. 6232088
 GENERAL INFORMATION:
 APPLICANT: Phairson Medical, Inc.
 APPLICANT: Richard L. Franklin
 APPLICANT: Yves St. Pierre
 TITLE OF INVENTION: Treatment and Prevention of Immune Rejection Reactions
 FILE REFERENCE: 314572-101D
 CURRENT APPLICATION NUMBER: US/09/220,731A
 CURRENT FILING DATE: 1998-12-24
 EARLIER APPLICATION NUMBER: PCT/SE93/00455
 EARLIER FILING DATE: 1993-05-21
 EARLIER APPLICATION NUMBER: 08/338,501
 EARLIER FILING DATE: 1994-11-22
 EARLIER APPLICATION NUMBER: 08/385,540
 EARLIER FILING DATE: 1995-02-08
 EARLIER APPLICATION NUMBER: 08/486,820
 EARLIER FILING DATE: 1995-06-07
 EARLIER APPLICATION NUMBER: 08/600,273
 EARLIER FILING DATE: 1996-02-08
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 23
 LENGTH: 178
 TYPE: PRT
 ORGANISM: Euphasia
 US-09-220-731-23

Query Match 98.6%; Score 136; DB 4; Length 178;
 Best Local Similarity 96.0%; Pred. No. 3.3e-14;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPQVQGLFIDDMYF 25
 Db 72 IVGGXEVTPHAYPQVQGLFIDDMYF 96

Search completed: May 30, 2003, 11:05:29
 Job time : 27 secs

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OM protein - protein search, using sw model.

Run on: May 30, 2003, 11:04:17 ; Search time 45 Seconds (without alignments)

56,235 Million cell updates/sec

Title: US-09-549-642-20

Perfect score: 138

Sequence: 1 IVGGMEVTPHAYPHQVGGLFDDMYF 25

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number of hits satisfying chosen parameters: 383519

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%, Maximum Match 100%

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3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US05_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	136	98.6	300	9 US-09-938-269-1	Sequence 1, Appli
2	101	73.2	25	9 US-09-938-269-2	Sequence 2, Appli
3	91	65.9	25	9 US-09-938-269-6	Sequence 6, Appli
4	89	64.5	25	9 US-09-938-269-7	Sequence 7, Appli
5	80	58.0	25	9 US-09-938-269-5	Sequence 5, Appli
6	75.5	54.7	970	10 US-09-888-615-101	Sequence 101, Appli
7	70	50.7	272	9 US-10-117-323-37	Sequence 37, Appli
8	69	50.0	271	9 US-10-117-323-39	Sequence 39, Appli
9	68	49.3	20	9 US-09-938-269-3	Sequence 3, Appli
10	67	48.6	252	9 US-10-117-323-38	Sequence 38, Appli
11	66	47.8	229	9 US-09-898-837A-53	Sequence 53, Appli
12	66	47.8	260	9 US-09-978-295A-395	Sequence 395, App
13	66	47.8	260	9 US-09-978-697-395	Sequence 395, App
14	66	47.8	260	9 US-09-978-192A-395	Sequence 395, App
15	66	47.8	260	9 US-09-999-832A-395	Sequence 395, App
16	66	47.8	260	9 US-09-978-189-395	Sequence 396, App
17	66	47.8	260	9 US-10-028-072-396	Sequence 396, App
18	66	47.8	260	9 US-10-121-049-396	Sequence 396, App
19	66	47.8	260	9 US-10-123-904-396	Sequence 396, App

ALIGNMENTS

RESULT 1 US-09-938-269-1

; Sequence 1, Application US-09938269

; Publication No. US20030007951A1

; GENERAL INFORMATION:

; APPLICANT: Franklin, Richard L.

; COWLING, Didier S.P.

; HUBBEL, Jeffrey A.

; APPLICANT: van de Wetering, Petra

; TITLE OF INVENTION: Treatment of Trauma

; FILE REFERENCE: 314572-105

; CURRENT APPLICATION NUMBER: US/09/938,269

; CURRENT FILING DATE: 2001-08-23

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 1

; LENGTH: 300

; TYPE: PRT

; ORGANISM: Panaeu vanamei

US-09-938-269-1

Query Match 98.6%; Score 136; DB 9; Length 300;

Best Local Similarity 96.0%; Pred. No. 5.1e-13;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 64 IVGSMEVTPHAYPHQVGGLFDDMYF 88

RESULT 2 US-09-938-269-2

; Sequence 2, Application US-09938269

; Publication No. US20030007951A1

; GENERAL INFORMATION:

; APPLICANT: Franklin, Richard L.

; COWLING, Didier S.P.

; HUBBEL, Jeffrey A.

; APPLICANT: van de Wetering, Petra

; TITLE OF INVENTION: Treatment of Trauma

; FILE REFERENCE: 314572-105

; CURRENT APPLICATION NUMBER: US/09/938,269

APPLICANT: Fernandes, Elina
 APPLICANT: Taupier Jr., Raymond
 APPLICANT: Rastelli, Luca
 APPLICANT: CurGen Corporation
 APPLICANT: Gerlach, Valerie L
 APPLICANT: Macdougal, John L
 TITLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN-KINASE LIKE PROTEINS AND NUCLEIC ACIDS ENCODING THE SAME
 FILE REFERENCE: 15966-598 CIP
 CURRENT APPLICATION NUMBER: US/09/898, 837A
 CURRENT FILING DATE: 2001-07-03
 PRIORITY NUMBER: U.S.S.N. 60/165,986
 PRIOR FILING DATE: 1999-11-17
 PRIORITY NUMBER: U.S.S.N. 60/194,839
 PRIOR FILING DATE: 2000-04-05
 PRIORITY NUMBER: U.S.S.N. 60/195,637
 PRIOR FILING DATE: 2000-04-07
 PRIORITY NUMBER: U.S.S.N. 60/197,080
 PRIOR FILING DATE: 2000-04-13
 PRIORITY NUMBER: U.S.S.N. 60/232,677
 PRIOR FILING DATE: 2000-09-15
 PRIORITY NUMBER: U.S.S.N. 60/181,347
 PRIOR FILING DATE: 2000-02-09
 PRIORITY NUMBER: U.S.S.N. 60/194,195
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 PRIORITY NUMBER: U.S.S.N. 60/215,906
 PRIOR FILING DATE: 2000-07-03
 PRIORITY NUMBER: U.S.S.N. 60/07791
 NUMBER OF SEQ ID NOS: 53
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 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-898-837A-53

Query Match 47 8%; Score 66; DB 9; Length 229;
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 Db 1 IVGGESALPCAWPQVSYQNVH 24

RESULT 12
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 Patent No. US20020156006A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J
 APPLICANT: Klaavins, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann

FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978, 697
CURRENT FILING DATE: 2001-10-16
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RESULT 14
 US-09-978-192A-395
 Sequence 395: Application US/09978192A
 Patent No. US2002017753A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Godowski, Paul J.
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillian, Kenneth J.
 APPLICANT: Kliavkin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2630PIC9
 CURRENT APPLICATION NUMBER: US/09/978,192A
 CURRENT FILING DATE: 2001-10-15
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Query Match 47.8%; Score 66; DB 9; Length 260;
Best Local Similarity 52.3%; Pred. NO. 0.021;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPMQVGLF 19
Db 33 VLGGHECPHSQPAALF 51

RESULT 15
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; Sequence 395, Application US/0999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; Applicant: Ashkenazi, Avi
; Applicant: Baker Kevin P.
; Applicant: Botstein, David
; Applicant: Desnoyers, Luc
; Applicant: Eaton, Dan
; Applicant: Ferraro, Napoleon
; Applicant: Filvaroff, Ellen
; Applicant: Fong, Sherman
; Applicant: Gao, Wei-Qiang
; Applicant: Gerber, Hans Peter
; Applicant: Gerritsen, Mary E.
; Applicant: Goddard, Audrey
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; Applicant: Grimaldi, J. Christopher
; Applicant: Gurney, Austin L.
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; Applicant: Kljavoin, Ivar J.
; Applicant: Kuo, Sophia S.
; Applicant: Napier, Mary A.
; Applicant: Pan, James
; Applicant: Paoni, Nicholas F.
; Applicant: Roy, Margaret Ann
; Applicant: Shelton, David L.
; Applicant: Stewart, Timothy A.
; Applicant: Tumas, Daniel
; Applicant: Williams, P. Mickey
; Applicant: Wood, William T.

; TITLE OF INVENTION: Secreted and transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P230PC63
; CURRENT APPLICATION NUMBER: US/09/999, 832A
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Query Match 47.88; Score 66; DB 9; Length 260;
Best Local Similarity 52.6%; Pred. No. 0.021; Matches 10; Conservatve 3; Mismatches 6; Indels 0; Gaps 0;

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Db 33 VLGGHECCPHSQFWQRAALF 51

Search completed: May 30, 2003, 11:13:13
Time : 46 secs

FT DISULFID 174 200 I -> V (IN REF. 1).
 FT CONFLICT 91 91 SN -> NS (IN REF. 1).
 FT CONFLICT 147 148 N -> D (IN REF. 1).
 FT CONFLICT 175 175 N -> D (IN REF. 1).
 FT CONFLICT 185 185 N -> D (IN REF. 1).
 SQ SEQUENCE 226 AA: 23511 MW: E45591CAF33CE8C CRC64:
 Query Match 64.58% Score 89; DB 1; Length 226;
 Best Local Similarity 64.0%; Pred. No. 3.1e-06;
 Matches 16; Conservative . 3; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 IVGGNEVTPHAYPHQWGLFDIDMYF 25
 Db 1 IVGGVEAVPNWSWPHQAAFLFDIDMYF 25
 SEQUENCE OF 29-53.
 STRAIN=Sprague-Dawley; TISSUE=Skin;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBITaxonID:10116;
 OC RN [1];
 OC RP SEQUENCE FROM N.A.
 OC RC STRAIN=Sprague-Dawley;
 OC RX MEDLINE=27149430; PubMed=89996238;
 OC RA Lutzelschw C.; Peijer G.; Aveskog M.; Hellman L.;
 OC RT "Secretory granule proteases and a carboxypeptidase A from various rat
 different serine proteases and a carboxypeptidase A from various rat
 mast cell populations";
 OC RL J. Exp. Med. 185:13-29 (1997).
 OC RN [2];
 OC RN [3];
 OC RP SEQUENCE OF 29-51.
 OC RC TISSUE=Breast carcinoma;
 OC MEDLINE=91242400; PubMed=2056367;
 OC RA Breganza V.J.; Simmons W.H.;
 OC RT "Tryptase from rat skin: purification and properties";
 OC RL Biochemistry 30:4997-5007 (1991).
 OC RN [4];
 OC RP SEQUENCE OF 29-51.
 OC RC TISSUE=Breast carcinoma;
 OC MEDLINE=92231826; PubMed=1314562;
 OC RA Eto I.; Grubbs C.J.;
 OC OS "Separation, purification and N-terminal sequence analysis of a novel
 RT leupeptin sensitive serine endopeptidase present in chemically
 induced rat mammary tumour";
 OC RT Biochem. J. 263:209-216 (1992).
 OC CC -1- FUNCTION: TRYPSIN IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST
 CELLS, AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION
 CC RESPONSE OF THIS CELL TYPE.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-, Lys-1-, but
 CC with more restricted specificity than trypsin.
 CC RL SUBUNIT: HOMOTRIMER.
 CC CC -1- SUBUNIT: HOMOTRIMER; RELEASED FROM THE SECRETORY GRANULES UPON
 CC -1- SUBCELLULAR LOCATION; RELEASED FROM THE SECRETORY GRANULES S1. TRYPSIN SUBFAMILY.
 CC CC -1- SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON
 CC -1- MAST CELL ACTIVATION.
 CC CC -1- TISSUE SPECIFICITY: MAST CELLS.
 CC CC -1- PTM: GLYCOSYLATED (PROBABLE).
 CC CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPSIN SUBFAMILY.
 CC CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
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 CC or send an email to license@isb-sib.ch).
 CC CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPSIN SUBFAMILY.
 CC DR EMBL: U67910; AAB48263; 1; -.
 CC DR PIR: A23698; A23698.
 CC DR PIR: A23698; A23698.
 CC DR HSSP: P20231; IAA0.
 CC DR MEROPS: S01.026; -.
 CC DR MEROPS: S01.143; -.
 CC DR InterPro: IPR001254; Ser_protease_Try.
 CC DR InterPro: IPR001254; Ser_protease_Try.
 CC DR PFAM: PF00089; trypsin_1.
 CC DR PROSITE: PS00240; TRYPSIN_DOM; PARTIAL.
 CC DR PROSITE: PS00134; TRYPSIN_HIS; PARTIAL.
 CC DR PROSITE: PS00135; TRYPSIN_SER; PARTIAL.
 CC DR PROSITE: PS00135; TRYPSIN_SER; 1.
 CC DR PROSITE: PS00135; TRYPSIN_SER; 1.
 CC KW Hydrolase: Serine protease; Glycoprotein; Zymogen; Signal;
 CC KW Multigene family.
 CC FT SIGNAL: 1. 18 POTENTIAL, PEPTIDE.
 CC FT PROPEP: 19 28 ACTIVATION PEPTIDE.
 CC FT CHAIN: 29 273 MAST CELL PROTEASE 7.
 CC FT ACT SITE: 72 72 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT ACT SITE: 119 119 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT ACT SITE: 222 222 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT DISULFID: 57 73 BY SIMILARITY.
 CC FT DISULFID: 153 228 BY SIMILARITY.
 CC FT DISULFID: 186 209 BY SIMILARITY.
 OC RESULT 5
 ID MCT7_RAT STANDARD; PRT: 273 AA.
 AC P27435; P27436;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DT Mast cell protease 7 precursor (EC 3.4.21.59) (RMCP-7) (Tryptase,
 DE skin).
 GN MCP7 OR MCP7.
 OS Rattus norvegicus (Rat).

FT	DISULFID	218	246	BY SIMILARITY.	FT	DISULFID	188	204	BY SIMILARITY.
FT	CARBOYD	49	49	N-LINKAGE (GLCNAC. . .) (PROBABLE).	FT	DISULFID	234	245	BY SIMILARITY.
FT	CONFLICT	42	42	W -> V (IN REF. 3).	FT	SEQUENCE	271	AA:	28313 MW; FA542AE38FFEB4B CRC64;
FT	CONFLICT	49	51	NDT -> WLP (IN REF. 3).	Query Match	50.0%	Score 69;	DB 1;	
SQ	SEQUENCE	273	AA:	30400 MW; 65A5ED4D279FB284 CRC64;	Best Local Similarity	61.1%	Pred. No. 0.0037;	Length 271;	
Query Match	50	78	Score 70;	DB 1;	Matches	11;	Conservative	3;	Mismatches 4;
Best Local Similarity	48	08	Pred. No. 0.0027;	Length 273;	Indels	0;	Gaps	0;	
Matches	12;	Conservative	6;	Mismatches 7;	Indels	0;	Gaps	0;	
QY	1	IVGGXEVTPHAYPWQVGLFDDMYF 25	QY	1	IVGGXEVTPHAYPWQVGL 18	Db	31	VVGGOBATPNTWPQVSL 48	
Db	29	IVGGQEASGNKWPQVSLRVNDTYW 53	RESULT 7						
RESULT 6			PLMN_SHEEP						
EL2_MOUSE			ID	PLMN_SHEEP					
ID	EL2_MOUSE		STANDARD;						
P05208;			PRT;	271 AA.					
13-AUG-1987		(Rel. 05, Created)							
13-AUG-1987		(Rel. 05, Last sequence update)							
15-JUN-2002		(Rel. 41, Last annotation update)							
DE	Elastase 2 precursor	(EC 3.4.21.71).							
GN	ELA2.								
OS	Mus musculus (Mouse).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
OX	NCBI_TaxID:10090;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	SEQUENCE ID:7066713; PubMed=3641189;								
RA	Stevenson B.J., Hagenbuechle O., Wellauer P.K.;								
RT	"Sequence organisation and transcriptional regulation of the mouse								
RT	elastase II and triptase genes."								
RL	Nucleic Acids Res. 14:3037-3130(1986).								
CC	-!- FUNCTION: ACTS UPON LASTIN.								
CC	-!- CATALYTIC ACTIVITY: Preferential cleavage: Leu- -xaa, Met- -xaa								
CC	and Phe- -xaa. Hydrolyzes elastin.								
CC	-!- SUBCELLULAR LOCATION: Secreted.								
CC	-!- TISSUE SPECIFICITY: PANCREAS.								
CC	-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.								
CC	-----								
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CC	use by non-profit institutions as long as its content is in no way								
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).								
EMBL	X04573; CAA8B242.1;								
DR	DR								
DR	PIR: X04576; CAA8B244.1;								
DR	PIR: A25528; A25528.								
DR	HSSP: P00072; 1ELG.								
DR	PRINTS: S01.155;								
DR	MGD: MGI:95316;								
DR	InterPro: IPR001314; Chymotrypsin.								
DR	InterPro: IPR001254; Ser-protease_tryp.								
DR	Pfam: PF00089; trypsin_1.								
DR	PRINTS: PR00072; CHYMOTRYPSIN.								
DR	SMART: SM00020;								
DR	PROSITE: PS050240; TRYSPN_SPC; 1.								
DR	PROSITE: PS00134; TRYSPN_DOM; 1.								
DR	PROSITE: PS00135; TRYSPN_LHS; 1.								
KW	KW Hydrolase; Serine protease; zymogen; signal.								
FT	SIGNAL	1	16	ACTIVATION PEPTIDE.	FT	NON_TER	1		
FT	PROPEP	17	30	ELASTASE 2.	FT	DOMAIN	<1	140	HEAVY CHAIN A.
FT	CHAIN	31	271	CHARGE RELAY SYSTEM (BY SIMILARITY).	FT	DOMAIN	141	>343	LIGHT CHAIN A.
FT	ACT_SITE	75	75	CHARGE RELAY SYSTEM (BY SIMILARITY).	FT	DOMAIN	<1	17	KRINGLE 4.
FT	ACT_SITE	123	123	CHARGE RELAY SYSTEM (BY SIMILARITY).	FT	DOMAIN	41	120	KRINGLE 5.
FT	DISULFID	218	76	BY SIMILARITY.	FT	DOMAIN	114	114	SERINE PROTEASE.

FT ACT-SITE 181 181	CHARGE RELAY SYSTEM.	SQ SEQUENCE 245 AA: 26260 MW: 74FE0D425517AB02 CRC64;
FT ACT-SITE 224 224	CHARGE RELAY SYSTEM.	
FT ACT-SITE 319 319	CHARGE RELAY SYSTEM.	
FT . NON-TER 343 343	CHARGE RELAY SYSTEM.	
SQ SEQUENCE 343 AA: 37662 MW: 8DF6EBA92D596EE0 CRC64;		
Query Match 50.0%: Score 69; DB 1; Length 343;		
Best Local Similarity 61.1%; Pred.: No. 0 0047; 3; Mismatches 4; Indels 0; Gaps 0;		
Matches 11; Conservative 3; Gaps 0;		
Qy 1 IVGGXEVTPHAYPWQVGL 18		
Db 114 VGGCVATPHSWPWQVSL 131		
RESULT 8		
CTRBL_GADMO ID CTRBL_GADMO STANDARD; PRT; 245 AA.		
AC P80461; AC P80461; AC P80461;		
DE 01-OCT-1996 (Rel. 34, Created)		
DE 15-JUN-2002 (Rel. 41, Last sequence update)		
Chymotrypsin B (EC 3.4.21.1).		
OS Gadus morhua (Atlantic cod).		
OC Eukarya; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC Actinopterygi; Neopterygi; Teleostei; Euteleostei; Neoteleostei;		
ACANTHOMORPHA: Paracanthopterygii; Gadiformes; Gadidae; Gadidae.		
NCBI-TAXID=8049; OX NCBI-TAXID=8049; OX NCBI-TAXID=8049;		
RN 11		
RP SEQUENCE.		
RC TISSUE=Pyloric caeca; RX MEDLINE=96139045; PubMed=8841380;		
RT morhua;"		
RA Leth-Larsen R., Asgeirsson B., Thorolfsson M., Noerregaard-Madsen M.,		
RA Hoejrup P.,		
RT "Structure of chymotrypsin variant B from Atlantic cod, <i>Gadus morhua</i> ;"		
RL Biochim. Biophys. Acta 1297:49-56(1996).		
RN 12		
RP SEQUENCE OF 1-12 AND 16-31.		
RC TISSUE=Pyloric caeca; RX MEDLINE=92111252; PubMed=1764912;		
RA Agarsrson B., Bjarnason J. B.		
RT "Structural and kinetic properties of chymotrypsin from Atlantic cod (<i>Gadus morhua</i>). Comparison with bovine chymotrypsin."		
RL Comp. Biochem. Physiol. 99B:327-335(1991).		
CC 1- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-1-Xaa, Trp-1-Xaa, Phe-1-Xaa, Leu-1-Xaa.		
CC -1- SIMILARITY: B1-M1, EXTRACELLULAR LOCATION: EXTRACELLULAR.		
CC -1- SIMILARITY: B1-M1, HSSP: P00766; ICHG: InterPro: IPR001314; Chymotrypsin.		
DR InterPro: IPR001314; Chymotrypsin.		
DR PRINTER: IPR001254; Ser_protease_TRY.		
DR PRINTS: PR00089; trypsin_1.		
DR SMART: SM0010; TrypSPC_1.		
DR PROSITE: PS00134; TRYPSIN_HIS_1.		
DR PROSITE: PS00135; TRYPSIN_SER_1.		
KW Hydrolyse; Serine protease; Pancreas; Zymogen.		
FT CHAIN 1 13 CHYMOTRYPSIN B, A CHAIN.		
FT CHAIN 16 245 CHYMOTRYPSIN B, B CHAIN.		
FT ACT-SITE 57 57 CHARGE RELAY SYSTEM (BY SIMILARITY).		
FT ACT-SITE 195 195 CHARGE RELAY SYSTEM (BY SIMILARITY).		
FT DISULFID 1 121 BY SIMILARITY.		
FT DISULFID 42 58 BY SIMILARITY.		
FT DISULFID 135 201 BY SIMILARITY.		
FT DISULFID 167 182 BY SIMILARITY.		
FT DISULFID 191 220 BY SIMILARITY.		
FT CONFLICT 9 11 QVT->VIS (IN REF. 2).		
FT CONFLICT 26 26 S->T (IN REF. 2).		
FT CONFLICT 28 29 PW->Y (IN REF. 2).		
RESULT 9		
CLCR_HUMAN ID CLCR_HUMAN STANDARD; PRT; 268 AA.		
AC Q99895; Q9NUH5; 000765; DE 16-OCT-2001 (Rel. 40, Created)		
DE 16-OCT-2001 (Rel. 40, Last sequence update)		
DE 16-OCT-2001 (Rel. 40, Last annotation update)		
DE Caldecrin precursor (EC 3.4.21.2) (Chymotrypsin C).		
GN CTRC OR CLCR.		
OS Homo sapiens (Human).		
OC Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
NCBI-TAXID=9606; OX NCBI-TAXID=9606;		
RN 11		
RP SEQUENCE FROM N.A., AND VARIANT TRP-80.		
RC TISSUE=Pancreas; RX MEDLINE=96221225; PubMed=8635596;		
RA Tomomura A., Akiyama M., Itoh H., Tomomura M., Nishii Y., Noikura T., Saneiki T.; RA RA		
RT "Molecular cloning and expression of human caldecrin."		
RL FEBS Lett. 386:26-28(1996).		
RN 12		
RP SEQUENCE FROM N.A.		
RC Coville G.; RA Coville G.; RA		
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.		
RN 13		
RP SEQUENCE OF 17-268 FROM N.A.		
RC TISSUE=Pancreas; Sziegoleit A.; RA Sziegoleit A.		
RT "A human pancreatic chymotrypsin: biochemical and molecular characterization."		
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.		
RN 14		
RP CHARACTERIZATION.		
RX MEDLINE=98207038; PubMed=9538241; RA YOSHINO-TASUDA I., Kobayashi K., Akiyama M., Itoh H., Tomomura A., SAHEKI T.; RA RA		
CC -1- "Caldecrin is a novel-type serine protease expressed in pancreas, but its homologue, elastase IV, is an artifact during cloning derived from caldecrin gene."		
CC -1- J. Biochem. 133:54-59(1998).		
CC -1- FUNCTION: HAS CHYMOTRYPSIN-TYPE PROTEASE ACTIVITY AND HYPOCALCEMIC ACTIVITY.		
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Leu-1-Xaa, Tyr-1-Xaa, Phe-1-Xaa, Met-1-Xaa, Trp-1-Xaa, Gln-1-Xaa, Asn-1-Xaa.		
CC -1- TISSUE SPECIFICITY: PANCREAS		
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.		
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CC DR EMBL; S82198; AAB47104-2; ALT_SEQ.		
CC DR EMBL; AL031283; CAB97355.1; DR EMBL; Y13697; CAA74031.1;		
CC DR HSSP; P00766; ICHG.		
CC DR MEROPS; S01.157; DR Genew; HGNC:2523; CTRC.		

MIM: 601405; -
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PRO0722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYPSIN_SPC; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR HSSP; AB038652; HSSP; 11AA0.
 KW Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal; Polymorphism.
 FT SIGNAL 1 16 POTENTIAL.
 FT PROPEP 17 29 ACTIVATION PEPTIDE.
 FT CHAIN 30 268 CALDECKIN.
 FT ACT_SITE 74 74 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 121 121 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 216 216 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 17 141 BY SIMILARITY.
 FT DISULFID 59 75 BY SIMILARITY.
 FT DISULFID 155 222 BY SIMILARITY.
 FT DISULFID 186 202 BY SIMILARITY.
 FT DISULFID 212 243 BY SIMILARITY.
 FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 80 80 R -> W.
 FT CONFLICT 16 16 S -> T (IN REF. 1).
 FT CONFLICT 52 52 N -> D (IN REF. 3).
 SQ SEQUENCE 268 AA: 29484 MW: 460BP33BA96516F CRC64;
 SQ SEQUENCE 9 50.0% Score 67; DB 1; Length 268;
 Best Local Similarity 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0; Matches 13; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
 Qy 1 IVGGXEVTPHAYPWQVGL 18
 Db 30 VVGGEDARPHSMWQIISL 47
 RESULT 10
 TRYPT_PIG STANDARD PRT; 275 AA.
 ID TRYPT_PIG ID: Q9N2D1; STANDARD; PRT; 275 AA.
 DT 16-OCT-2001 (Rel. 40, Created)
 DR 15-JUN-2002 (Rel. 41, Last sequence update)
 DR TRYPTase precursor (EC 3.4.21.59).
 DR MCT7.
 OC Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC NCBI_TaxID=9823;
 RN [1] SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=20385343; PubMed=10824103;
 RA Chen Y., Shioya M., Ohuchi M., Towatari T., Tashiro J., Murakami M., Yano M., Yang B., Kido H.;
 RT "Mast cell tryptase from pig lungs triggers infection by pneumotropic Sendai and influenza A viruses. Purification and characterization." Eur. J. Biochem. 267:3189-3197 (2000).
 CC -!- FUNCTION: TRYPTASE IS THE MAJOR NEUTRAL PROTEASE PRESENT IN MAST CELLS AND IS SECRETED UPON THE COUPLED ACTIVATION-DEGRANULATION RESPONSE OF THIS CELL TYPE.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-, Lys-1-, but with more restricted specificity than trypsin.
 CC -!- SUBUNIT: HOMOTRIMER (By similarity).
 CC -!- SUBCELLULAR LOCATION: RELEASED FROM THE SECRETORY GRANULES UPON MAST CELL ACTIVATION.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
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 CC -!- EMBL; AB038652; HSSP; P20231; 11AA0.
 DR MEROPS; S01.143; -.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PRO0722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYPSIN_SPC; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen.
 FT SIGNAL 1 20 ACTIVATION PEPTIDE (BY SIMILARITY).
 FT PROPEP 21 30 TRYPTASE.
 FT CHAIN 31 275 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 74 74 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 121 121 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 216 216 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 17 141 BY SIMILARITY.
 FT DISULFID 59 75 BY SIMILARITY.
 FT DISULFID 155 222 BY SIMILARITY.
 FT DISULFID 186 202 BY SIMILARITY.
 FT DISULFID 212 243 BY SIMILARITY.
 FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 80 80 R -> W.
 FT CONFLICT 16 16 S -> T (IN REF. 1).
 FT CONFLICT 52 52 N -> D (IN REF. 3).
 SQ SEQUENCE 268 AA: 29484 MW: 460BP33BA96516F CRC64;
 SQ SEQUENCE 9 50.0% Score 67; DB 1; Length 268;
 Best Local Similarity 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0; Matches 13; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
 Qy 1 IVGGXEVTPHAYPWQVGL 25
 Db 31 IVGGKEAPGKHWPMWQVSLRCLDQYW 55
 RESULT 11
 KLK8_HUMAN STANDARD PRT; 260 AA.
 ID KLK8_HUMAN STANDARD; PRT; 260 AA.
 AC 060259; Q9UQ47; Q9UQ53; Q9UQ59;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DT Neurokinin precursor (EC 3.4.21.7) (NP) (Kallikrein 8) (Ovasin) (Serine protease_TADG14) (tumor-associated differentially expressed gene-14 protein).
 DE PRT; TADG14 OR NRNP.
 DE KLK8 OR PRSS19 OR TADG14 OR NRNP.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBITaxID=9606;
 RN [1] SEQUENCE FROM N.A. (ISOFORM 1).
 RP TISSUE=Hippocampus; PubMed=9714609;
 RC MEDLINE=98372070; PubMed=9714609;
 RX Yoshiida S., Taniguchi M., Hirata A., Shiosaka S.;
 RT "Sequence analysis and expression of human neurokinin cDNA and gene." Gene 213:9-16 (1998).
 RN [2] SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RP TISSUE=Brain; PubMed=10102990;
 RC MEDLINE=99203457; PubMed=10102990;
 RA Mitsui S., Tsuruoka N., Yamashiro K., Nakazato H., Yamaguchi N.;
 RT "A novel form of human neurokinin, a brain-related serine protease, is generated by alternative splicing and is expressed preferentially in human adult brain." Eur. J. Biochem. 260:627-634 (1999).
 RL

RN	[3]	SEQUENCE FROM N.A. (ISOFORM 1).	DR	SMART: SM00020; TRYPSIN_SPC; 1.
RC		TISSUE:ovary;	DR	PROSITE; PS50240; TRYPSIN_DOM; 1.
RA	MEDLINE:99413504; Pubmed=1048549;		DR	PROSITE; PS00134; TRYPSIN_HIS; 1.
RA	Underwood L.J., Tanimoto H., Wang Y., Shigemasa K., Parmley T.H., O'Brien T.J.;		DR	PROSITE; PS00135; TRYPSIN_SER; 1.
RA	"Cloning of tumor-associated differentially expressed gene-14, a novel serine protease overexpressed by ovarian carcinoma.";		KW	Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal; Alternative splicing.
RT			FT	SIGNAL 1
RL	Submitted (SEP-1998) to the EMBL/Genbank/DBJ/Genbank/DBJ databases.		FT	PROPEP 28
RN	[4]	SEQUENCE FROM N.A. (ISOFORM 1).	FT	PROPEP 29
RP	Gan L., Gellins R., Gown A.M., Moss P., Smith R., Wang K.;		FT	CHAIN 32
RA	"Molecular cloning and characterization of a novel serine protease, ovasin, a potential molecular marker for ovarian carcinomas.";		FT	CHAIN 33
RT	Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.		FT	NEUROPSIN.
RL			FT	ACT SITE 73
RN	[5]	SEQUENCE FROM N.A. (ISOFORM 1).	FT	ACT SITE 73
RP	MEDLINE:20510030; Pubmed=11054574;		FT	ACT SITE 120
RA	Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,		FT	ACT SITE 212
RA	Moss P., Paepke B., Wang K.;		FT	DISULFID 39
RA	"Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";		FT	DISULFID 58
RA	Gene 257:119-130 (2000).		FT	DISULFID 74
RN	[6]	SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).	FT	DISULFID 145
RA	Leinwand J.E., McCready P.M., Skowronski E., Viswanathan V., Burkhardt-Schultz K., Gordon L., Diaz J.J., Ramirez M., Stilwagen S.,		FT	DISULFID 152
RA	Burkhardt-Schultz K., Gordon L., Diaz J.J., Ramirez M., Stilwagen S.,		FT	DISULFID 184
RA	Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.J.,		FT	DISULFID 208
RA	Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S., Andreise T., Frankheim M., Attix C., Amico-Keller G., Coiffield J.,		FT	CARBOHYD 110
RA	Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.;		FT	CARSPLIC 23
RA	"Sequence analysis of chromosome 19q13.4.";		FT	WRSPMLPAA (IN ISOFORM 2).
RL	Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.		SQ	SEQUENCE 260 AA: EF43965BB8C3E660 CRC64;
CC	-1- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND HIPPOCAMPAL PLASTICITY.		Query	Match 47.8%; Score 66; DB 1; Length 260;
CC			Best Local Similarity 52.6%; Pred. No. 0.01;	
CC	-1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-; LYS-.		Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	
CC			Qy 1 IYQXEXVTPHAYPQVQGLF 19	
CC	-1- SUBCELLULAR LOCATION: Secreted.		Db 33 VLGGHECQPHSQPMQAALF 51	
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPlicing.			
CC	-1- TISSUE SPECIFICITY: ISOFORM 1 IS PREDOMINANTLY EXPRESSED IN THE PANCREAS WHILE ISOFORM 2 IS EXPRESSED IN ADULT BRAIN AND HIPPOCAMPUS. BOTH FORMS ARE ALSO FOUND IN FETAL BRAIN AND PLACENTA. NOT DETECTED IN KIDNEY, SPLEEN, LIVER AND LUNG.			
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, KALLIKREIN SUBFAMILY.			
CC				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC				
DR	EMBL: AB009849; BAA28673.1; [2]		RP	SEQUENCE FROM N.A.
DR	EMBL: AB012761; BAA28676.1; [2]		RX	MEDLINE:85054882; PubMed=6094548;
DR	EMBL: AB010750; BAA28684.1; [2]		RA	Swift G.H., Craik C.S., Stary S.J., Quinto C., Lahate R.G., McDonald R.J., Swift G.H., Quinto C., Swain W., Pictet R.L., Rutter W.J., Macdonald R.J.;
DR	EMBL: AB008390; BAA28684.1; [2]		RA	"Structure of the two related elastase genes expressed in the rat pancreas.";
DR	EMBL: AB008927; BAA28666.1; [2]		RT	RT
DR	EMBL: AB0055982; AAD56050.1; [2]		RL	Rattus norvegicus (Rat); Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathini; Murinae; Rattus; NCBI_TaxID=10116;
DR	EMBL: AF095742; AAD25979.1; [2]		RL	Biochemistry 21:1453-1463(1982).
DR	EMBL: AF095743; AAD29574.1; [2]		RN	[1]
DR	EMBL: AF243527; AAG3361.1; [2]		RP	SEQUENCE FROM N.A.
DR	EMBL: ACO1143; AAG23254.1; [2]		RX	MEDLINE:82182967; PubMed=6918221.
DR	HSSP: Q61955; 1NPBM.		RA	McGovits W., Rutter W.J.;
DR	MEROPS: S01_244.		RA	"Primary structure of two distinct rat pancreatic preproelastases determined by sequence analysis of the complete cloned messenger ribonucleic acid sequences.";
DR	Genew: HGNC:6369; KLKB.		RT	RT
DR	MIM: 601644; [2]		CC	-1- FUNCTION: ACTS UPON ELASTIN.
DR	InterPro: IPR001314; Chymotrypsin.		CC	-1- CATALYTIC ACTIVITY: Preferential cleavage: Leu-1-Xaa, Met-1-Xaa and Phe-1-Xaa. Hydrolyzes elastin.
DR	InterPro: IPR01254; Ser_protease_tryp.		CC	-1- SUBCELLULAR LOCATION: Secreted.
DR	PRINTS: PR00089; trypsin; 1.		CC	-1- TISSUE SPECIFICITY: PANCREAS.
DR	PRINTS: PR00722; CHYMOTRYPSIN.		CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.
CC			CC	
CC			CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way

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.....

EMBL; VOL233; CAA24543.1; -.

EMBL; L00124; AAA98780.1; -.

EMBL; L00118; AAA98780.1; JOINED.

EMBL; L00119; AAA98780.1; JOINED.

EMBL; L00120; AAA98780.1; JOINED.

EMBL; L00121; AAA98780.1; JOINED.

EMBL; L00122; AAA98780.1; JOINED.

EMBL; L00123; AAA98780.1; JOINED.

PIR; A00961; ELR2.

HSSP; P00772; 1EUG.

MEIOPS; S01_155.

InterPro; IPR001214; Chymotrypsin.

InterPro; IPR001214; Ser_protease_TRY.

PRINTS; PRO0722; CHYMOTRYPSIN.

SMART; SM00020; TRY_SPc_1.

PROSITE; PS50240; TRYPSIN_DOM_1.

PROSITE; PS00134; TRYPSIN_HIS_1.

PROSITE; PS00135; TRYPSIN_SER_1.

Hydrolase; Serine_Protease_2; yrogen; Signal.

SIGNAL; 1 16 ACTIVATION PEPTIDE.

PROPEP; 17 30 ELASTASE_2.

CHAIN; 31 271 CHARGE_RELAY_SYSTEM (BY SIMILARITY).

ACT_SITE; 75 75 CHARGE_RELAY_SYSTEM (BY SIMILARITY).

ACT_SITE; 123 123 CHARGE_RELAY_SYSTEM (BY SIMILARITY).

ACT_SITE; 218 218 CHARGE_RELAY_SYSTEM (BY SIMILARITY).

DISULFID; 60 76 BY SIMILARITY.

DISULFID; 157 224 BY SIMILARITY.

DISULFID; 188 204 BY SIMILARITY.

DISULFID; 214 245 BY SIMILARITY.

SEQUENCE; 271 AA; 28885 MW; 125C783B857B71E3 CRC64;

Query Match Score 66; DB 1; Length 271;

Best Local Similarity 47.8%; Pred. No. 0.01;

Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

1 IVGGXEVTPHAPWQVGL 18

31 VVGGQEASPNWQVSL 48

.....

RESULT 1.3

TMS2_HUMAN STANDARD; PRT; 492 AA.

015393; Q9BAX1; 15-JUL-1998 (Rel. 36, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Transmembrane protease, serine 2 precursor (EC 3.4.21.-).

TMRSS2 OR PRSS10.

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TAXID 9606;

[1] SEQUENCE FROM N.A.

MEDLINE-97168144; PubMed-9325052;

Paoloni-Giacobino A., Chen H., Peitsch M.C., Rossier C., Antonarakis S.E.;

"Cloning of the TMRSS2 gene, which encodes a novel serine protease with transmembrane, LDLRA, and SRCR domains and maps to 21q22.3.";

Genomics 44:309-320(1997).

[2] SEQUENCE FROM N.A.

MEDLINE-21090969; PubMed-11414763;

Teng D.H., Chen Y., Lian L., Ha P.C., Tavtigian S.V., Wong A.K.; "Mutation analysis of 268 candidate genes in human tumor cell lines.";

Genomics 74:352-364(2001).

FT	DISULFID	172	231	BY SIMILARITY.	RESULT 15
FT	DISULFID	185	241	INTERCHAIN (BY SIMILARITY).	GRAA_HUMAN
FT	DISULFID	244	365	BY SIMILARITY.	ID GRAA_HUMAN
FT	DISULFID	281	297	BY SIMILARITY.	STANDARD; PRT; 262 AA.
FT	DISULFID	410	426	BY SIMILARITY.	AC P12544;
FT	DISULFID	437	465	BY SIMILARITY.	DT 01-OCT-1989 (Rel. 12, Created)
FT	CARBOHYD	213	213	N-LINKED (GLCNAC. . .) (POTENTIAL).	DT 01-OCT-1989 (Rel. 12, Last sequence update)
FT	CARBOHYD	249	249	N-LINKED (GLCNAC. . .) (POTENTIAL).	DT 15-JUN-2002 (Rel. 41, Last annotation update)
FT	VARIANT	449	449	K -> N (IN DBSNP:1056602).	DE Granzyme A precursor (EC 3.4.21.78) (Cytotoxic T-lymphocyte proteinase DE 1) (Hanukkuk factor) (H factor) (HF) (Granzyme 1) (CTL tryptase DE 1) (Hanukkuk 1).
FT	MUTAGEN	255	255	/ETID=VAR_011692.	DE (Fragment 1).
FT	MUTAGEN	441	441	R->Q: LOSS OF CLEAVAGE.	GN GZMA OR CTLA3 OR HFSP.
FT	CONFFLICT	160	160	S->A: LOSS OF ACTIVITY.	OS Homo sapiens (Human).
FT	CONFFLICT	242	242	M -> V (IN REF. 3).	RT Cloning and chromosomal assignment of a human cDNA encoding a T cell- and natural killer cell-specific trypsin-like serine protease.
FT	CONFFLICT	329	329	I -> L (IN REF. 1).	OC Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
FT	CONFFLICT	489	491	E -> Q (IN REF. 1).	OC Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
FT	SEQUENCE	492 AA;	53891 MW;	RAD -> KAN (IN REF. 1).	NCBI_TaxID=9606;
FT	SEQUENCE	492 AA;	53891 MW;	CAB44FD174A9076B CRC64;	RN [1]
FT	SEQUENCE	492 AA;	53891 MW;	RA SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
FT	SEQUENCE	492 AA;	53891 MW;	RC TISSUE-Blood;	RC TISSUE-Blood;
FT	SEQUENCE	492 AA;	53891 MW;	RA Strausberg R.;	RC Strausberg R.;
FT	SEQUENCE	492 AA;	53891 MW;	RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.	RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
FT	SEQUENCE	492 AA;	53891 MW;	RN [13]	RN [13]
FT	SEQUENCE	492 AA;	53891 MW;	RP SEQUENCE OF 1-23 FROM N.A.	RP SEQUENCE OF 1-23 FROM N.A.
FT	SEQUENCE	492 AA;	53891 MW;	RA Goralski T.J., Krensky A.M.;	RA Goralski T.J., Krensky A.M.;
FT	SEQUENCE	492 AA;	53891 MW;	RT "The upstream region of the human granzyme A locus contains both positive and negative transcriptional regulatory elements."	RT "The upstream region of the human granzyme A locus contains both positive and negative transcriptional regulatory elements."
FT	SEQUENCE	492 AA;	53891 MW;	RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.	RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
FT	SEQUENCE	492 AA;	53891 MW;	RN [14]	RN [14]
FT	SEQUENCE	492 AA;	53891 MW;	RP SEQUENCE OF 29-53.	RP SEQUENCE OF 29-53.
FT	SEQUENCE	492 AA;	53891 MW;	RA Poe M., Bennett C.D., Biddison W.E., Blake J.T., Norton G.P.,	RA Poe M., Bennett C.D., Biddison W.E., Blake J.T., Norton G.P.,
FT	SEQUENCE	492 AA;	53891 MW;	RA Rodkey J.A., Sigal N.H., Turner R.V., Wu J.K., Zweerink H.J.;	RA Rodkey J.A., Sigal N.H., Turner R.V., Wu J.K., Zweerink H.J.;
FT	SEQUENCE	492 AA;	53891 MW;	RT Human cytotoxic lymphocyte trypsinase. Its purification from granules and the characterization of inhibitor and substrate specificity.	RT Human cytotoxic lymphocyte trypsinase. Its purification from granules and the characterization of inhibitor and substrate specificity.
FT	SEQUENCE	492 AA;	53891 MW;	RL J. Biol. Chem. 263:13215-13222(1988).	RL J. Biol. Chem. 263:13215-13222(1988).
FT	SEQUENCE	492 AA;	53891 MW;	RN [15]	RN [15]
FT	SEQUENCE	492 AA;	53891 MW;	RP SEQUENCE OF 29-40, AND CHARACTERIZATION.	RP SEQUENCE OF 29-39, AND CHARACTERIZATION.
FT	SEQUENCE	492 AA;	53891 MW;	RP MEDLINE=89009866; PubMed=2262682;	RP MEDLINE=89009866; PubMed=2262682;
FT	SEQUENCE	492 AA;	53891 MW;	RA Hameed A., Lowrey D.M., Lichtenheld M., Podack E.R.;	RA Hameed A., Lowrey D.M., Lichtenheld M., Podack E.R.;
FT	SEQUENCE	492 AA;	53891 MW;	RT "Characterization of three serine esterases isolated from human IL-2 activated killer cells."	RT "Characterization of three serine esterases isolated from human IL-2 activated killer cells."
FT	SEQUENCE	492 AA;	53891 MW;	RL J. Immunol. 141:3142-3147(1988).	RL J. Immunol. 141:3142-3147(1988).
FT	SEQUENCE	492 AA;	53891 MW;	RN [16]	RN [16]
FT	SEQUENCE	492 AA;	53891 MW;	RP SEQUENCE OF 29-39, AND CHARACTERIZATION.	RP SEQUENCE OF 29-39, AND CHARACTERIZATION.
FT	SEQUENCE	492 AA;	53891 MW;	RP MEDLINE=89035468; PubMed=2263427;	RP MEDLINE=89035468; PubMed=2263427;
FT	SEQUENCE	492 AA;	53891 MW;	RA Kraehenbuhl O., Rey C., Jenne D.E., Lanzavecchia A., Grosscurth P.,	RA Kraehenbuhl O., Rey C., Jenne D.E., Lanzavecchia A., Grosscurth P.,
FT	SEQUENCE	492 AA;	53891 MW;	RA Carel S., Tschopp J.;	RA Carel S., Tschopp J.;
FT	SEQUENCE	492 AA;	53891 MW;	RT "Characterization of granzymes A and B isolated from granules of cloned human cytotoxic T lymphocytes."	RT "Characterization of granzymes A and B isolated from granules of cloned human cytotoxic T lymphocytes."
FT	SEQUENCE	492 AA;	53891 MW;	RL J. Immunol. 141:3471-3477(1988).	RL J. Immunol. 141:3471-3477(1988).
FT	SEQUENCE	492 AA;	53891 MW;	RN [17]	RN [17]
FT	SEQUENCE	492 AA;	53891 MW;	RP 3D-STRUCTURE MODELING.	RP 3D-STRUCTURE MODELING.
FT	SEQUENCE	492 AA;	53891 MW;	RP MEDLINE=89184501; PubMed=3237717;	RP MEDLINE=89184501; PubMed=3237717;
FT	SEQUENCE	492 AA;	53891 MW;	RA Murphy M.E.P., Moulit J., Bleackley R.C., Gershengenfeld H.,	RA Murphy M.E.P., Moulit J., Bleackley R.C., Gershengenfeld H.,
FT	SEQUENCE	492 AA;	53891 MW;	RA Weissman I.L., James M.N.G.;	RA Weissman I.L., James M.N.G.;
FT	SEQUENCE	492 AA;	53891 MW;	RT Comparative molecular model building of two serine proteinases from cytotoxic T lymphocytes.	RT Comparative molecular model building of two serine proteinases from cytotoxic T lymphocytes.
FT	SEQUENCE	492 AA;	53891 MW;	RA Proteins 4:190-204 (1988).	RA Proteins 4:190-204 (1988).
FT	SEQUENCE	492 AA;	53891 MW;	CC -!- FUNCTION: THIS ENZYME IS NECESSARY FOR TARGET CELL LYSIS IN CELL-MEDIATED IMMUNE RESPONSES.	CC -!- FUNCTION: THIS ENZYME IS NECESSARY FOR TARGET CELL LYSIS IN CELL-MEDIATED IMMUNE RESPONSES.
FT	SEQUENCE	492 AA;	53891 MW;	CC INVOLVED IN APOPTOSIS.	CC INVOLVED IN APOPTOSIS.
FT	SEQUENCE	492 AA;	53891 MW;	CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins, including fibronectin, type IV collagen and nucleolin. Preferential cleavage: Arg-1-xaa, Lys-1-xaa>> Phe-1-xaa in small molecule substrates.	CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins, including fibronectin, type IV collagen and nucleolin. Preferential cleavage: Arg-1-xaa, Lys-1-xaa>> Phe-1-xaa in small molecule substrates.
FT	SEQUENCE	492 AA;	53891 MW;	CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.	CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.

CC -1 SUBCELLULAR LOCATION: CYTOPLASMIC GRANULES
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, GRANZYME SUBFAMILY.
 CC
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 DR EMBL: M18737; AA52647; 1.
 DR EMBL: EBC015739; AAH15739; 1.
 DR EMBL: U40006; AA0009; 1.
 DR PIR: A28943; A28943.
 DR PIR: A30525; A30525.
 DR PIR: A30526; A30526.
 DR PIR: A31372; A31372.
 DR PDB: 1HFL; 15-OCT-94.
 DR MEROPS: S01.135;
 Genew; HGNC:4708; GZMA.
 MM: 140050.
 DR InterPro; IPR01254; Ser_protease_Try.
 DR Pfam; PF00089; trypsin; 1.
 DR SMART; SM00020; TRYSP; SPC; 1.
 DR PROSITE; PS03020; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolyse; Serine protease; Zymogen; Signal; T-cell; Cytolysis;
 KW Apoptosis; 3D-structure.
 SIGNAL 1 26
 FT PROPEP 27 28 ACTIVATION PEPTIDE.
 FT CHAIN 29 262 GRANZYME A.
 FT ACT_SITE 69 69 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 114 114 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 212 212 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 54 70 BY SIMILARITY.
 FT DISULFID 148 218 BY SIMILARITY.
 FT DISULFID 179 197 BY SIMILARITY.
 FT DISULFID 208 234 BY SIMILARITY.
 FT CARBOHYD 170 170 N-LINKED (GLUCNAC, ...) (POTENTIAL).
 SQ SEQUENCE 262 AA; 28968 MW; DA87563A0D92BAF4 CR064;

Query Match 47.1% Score 65; DB 1; Length 262;

Best Local Similarity 57.1%; Pred. No. 0.014; Mismatches 5; Indels 0; Gaps 0;

1 IVGGXETPHAYPWQVGFID 21
 1:1:1 1:1:1: 1: 1: 1:
 29 IIGGNEYTPHSRPMVLLSLD 49

Search completed: May 30, 2003, 11:02:43
 Job time : 23 secs

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OM protein - protein search, using sw model

Run on: May 30, 2003, 10:57:47 ; Search time 79 Seconds (without alignments)

65.205 Million cell updates/sec

Title: US-09-549-642-20

Perfect score: 138

Sequence: 1 IVGXXEVTPHAYPNQVGLFIDDMYF 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

1 number of hits satisfying chosen parameters: 671580

1 minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriopl:*

17: sp_archeap:*

ALIGNMENTS

Result No.	Score	Query	Match	Length	DB	ID	Description
1	101	73.2	271	5	018487	018487 penaeus van	018487 penaeus van
2	95	68.8	270	5	08WFL1	08WFL1 parathiole	08WFL1 parathiole
3	94	68.1	265	5	018488	018488 penaeus van	018488 penaeus van
4	89	64.5	270	5	Q27824	027824 uca pugilat	027824 uca pugilat
5	77	55.8	254	6	Q9XSN6	09XSN6 sus scrofa	09XSN6 sus scrofa
6	76	55.1	474	5	Q8T4N3	Q8T4N3 hippocampus	Q8T4N3 hippocampus
7	74	53.6	309	5	Q27083	Q27083 tachypodus	Q27083 tachypodus
8	72	52.2	255	11	Q9Z0M1	09Z0M1 mus musculus	09Z0M1 mus musculus
9	72	52.2	255	11	Q931S2	0931S2 mus musculus	0931S2 mus musculus
10	72	52.2	270	5	096871	096871 trichinella	096871 trichinella
11	71	51.4	465	5	Q9BAL7	Q9BAL7 trichinella	Q9BAL7 trichinella
12	69	50.0	467	5	Q967X8	Q967X8 panulirus a	Q967X8 panulirus a
13	69	50.0	868	13	Q9TIV3	Q9TIV3 polyandrosa	Q9TIV3 polyandrosa
14	69	50.0	1524	13	Q91674	Q91674 xenopus lae	Q91674 xenopus lae
15	67	48.6	263	13	Q9PWQ6	Q9PWQ6 gadus morhua	Q9PWQ6 gadus morhua
16	66	47.8	260	13	Q9w7Q3	Q9w7Q3 paralichthys	Q9w7Q3 paralichthys

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	101	73.2	271	5	018487	018487 penaeus van	018487 penaeus van
2	95	68.8	270	5	08WFL1	08WFL1 parathiole	08WFL1 parathiole
3	94	68.1	265	5	018488	018488 penaeus van	018488 penaeus van
4	89	64.5	270	5	Q27824	027824 uca pugilat	027824 uca pugilat
5	77	55.8	254	6	Q9XSN6	09XSN6 sus scrofa	09XSN6 sus scrofa
6	76	55.1	474	5	Q8T4N3	Q8T4N3 hippocampus	Q8T4N3 hippocampus
7	74	53.6	309	5	Q27083	Q27083 tachypodus	Q27083 tachypodus
8	72	52.2	255	11	Q9Z0M1	09Z0M1 mus musculus	09Z0M1 mus musculus
9	72	52.2	255	11	Q931S2	0931S2 mus musculus	0931S2 mus musculus
10	72	52.2	270	5	096871	096871 trichinella	096871 trichinella
11	71	51.4	465	5	Q9BAL7	Q9BAL7 trichinella	Q9BAL7 trichinella
12	69	50.0	467	5	Q967X8	Q967X8 panulirus a	Q967X8 panulirus a
13	69	50.0	868	13	Q9TIV3	Q9TIV3 polyandrosa	Q9TIV3 polyandrosa
14	69	50.0	1524	13	Q91674	Q91674 xenopus lae	Q91674 xenopus lae
15	67	48.6	263	13	Q9PWQ6	Q9PWQ6 gadus morhua	Q9PWQ6 gadus morhua
16	66	47.8	260	13	Q9w7Q3	Q9w7Q3 paralichthys	Q9w7Q3 paralichthys

RESULT 1	018487	ID	018487	PRELIMINARY;	PRT;	271 AA.
	AC	018487,		(TREMBLrel. 05, Created)		
	DT	01-JAN-1998		(TREMBLrel. 05, Last sequence update)		
	DT	01-JUN-2002		(TREMBLrel. 21, Last annotation update)		
	DE	Chymotrypsin BI (Fragment).				
	GN	CHYMOTRYPSIN A.				
	OS	Penaeus vannamei. (Penaeid shrimp) (European white shrimp).				
	OC	Eukaryota; Metazoa; Eucarya; Crustacea; Malacostraca;				
	OC	Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;				
	NCBI_TAXID	=6689;				
RN		(1)				
RP		SEQUENCE FROM N_A.				
RC		TISSUE-SPERMATOPHORUS;				
RX		MEDLINE-99331490; PubMed-10407165;				
RT		Sellios D.Y., Van Wommelk A;				
RT		"Polymorphism and evolution of collagenolytic serine protease genes in crustaceans."				
RL		Blockchin, Biophys. Acta 1432:419-424 (1999).				
CC		-1. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS "THE TRYPsin FAMILY".				
CC		EMBL: Y10664; CAA71672.1; -.				
DR		HSSP; P00771; IAVZ.				
DR		MEPROPS; S01_122; -.				
DR		InterPro: IPR001314; Chymotrypsin.				
DR		InterPro: IPR001254; Ser_protease_Try.				
DR		PFAM: PF00899; trypsin_1.				
DR		PRINTS: PRO00722; CHYMOTRYPSIN.				
DR		SMART; SM00020; Tryp_SPC; 1.				
DR		PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.				
DR		PROSITE; PS00135; TRYPSIN_SER; 1.				
KW		Hydrolyase; Serine protease.				
FT		NON_TER 271 AA;				
SQ		SEQUENCE 271 AA; 28743 MW; EAD3F41DD6053ADE CRC64;				

RESULT 5							
Q9XSN6	PRELIMINARY;	PRT;	254 AA.				
AC							
ID Q9XSN6;							
DT 01-NOV-1999 (TREMBLrel. 12, Created)							
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)							
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)							
DE Enamel matrix serine proteinase 1 precursor.							
OS Sus scrofa (Pig)							
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Sulina; Sulidae; Sus.							
NCBI_TaxID=9823;							
RN [1]							
RP SEQUENCE FROM N.A.							
RX MEDLINE=98126310;							
RA Summer J.P., Fukae M., Tanabe T., Yamakoshi Y., Uchida T., Xue J., Margolis H.C., Shimizu M., DeHart B.C., Hu C.-C., Bartlett J.D.;							
PE Purification, characterization, and cloning of enamel matrix serine proteinase 1.							
J. Dent. Res. 77: 377-386 (1998).							
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPsin FAMILY.							
CC EMBL; U06256; AA094638.1; -.							
DR HSSP; P00763; 10PO.							
DR MEROPS; S01_251; -.							
DR MEROPS; S01_251; -.							
DR InterPro; IPR001314; Chymotrypsin.							
DR InterPro; IPR001254; Serine_protease_Try.							
DR Pfam; PF00089; Trypsin.							
DR SMART; SM00022; CHYMOTRYPSIN.							
DR SMART; SM00020; TRYPSIN_SPC.							
DR PROSITE; PS00240; TRYPSIN_DOM; 1.							
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.							
DR PROSITE; PS00135; TRYPSIN_SER; 1.							
KW Hydrolase; Serine protease; Signal.							
FT SIGNAL 1 24 POTENTIAL.							
FT CHAIN 31 254 ENAMEL MATRIX SERINE PROTEINASE 1.							
SEQUENCE 254 AA; 27235 MW; FD40EEF85664406FT CRC64;							
Query Match 55.8%; Score 77; DB 6; Length 254;							
Best Local Similarity 44.08%; Pred. No. 0.0013; Indels 0; Gaps 0;							
Matches 11; Conservative 6; Mismatches 8; Indels 0; Gaps 0;							
Qy 1 IVGGXEVTPHAYPWNQVGLFIDDMYF 25							
Db 31 IINGEDCNPHSQWAALFLEDDFF 55							
QT 6							
N3 Q8T4N3	PRELIMINARY;	PRT;	474 AA.				
AC							
ID Q8T4N3;							
DT 01-JUN-2002 (TREMBLrel. 21, Created)							
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)							
DE Midgut serine proteinase-2.							
OS Rhipicephalus appendiculatus (Brown ear tick).							
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari; Parasitiformes; Ixodida; Ixodidae; Rhipicephalidae.							
NCBI_TaxID=24631;							
RN [1]							
RP SEQUENCE FROM N.A.							
RX "Rhipicephalus appendiculatus midgut serine proteinase-2, cDNA cloning and characterization"; Submitted (PEB-2002) to the EMBL/GenBank/DBJ databases.							
DR EMBL; AY078094; AAL70566.1; -.							
SEQUENCE 474 AA; 51232 MW; B013301E1F00EF49F CRC64;							
Query Match 55.1%; Score 76; DB 5; Length 474;							
Best Local Similarity 66.78%; Pred. No. 0.0036; Indels 3; Mismatches 3; Gaps 0;							
Qy 1 IVGGXEVTPHAYPWNQVGLF 19							
Db 47 IGGGATPHSNWVMGIF 65							
RESULT 8							
Q9Z0M1	PRELIMINARY;	PRT;	255 AA.				
AC							
ID Q9Z0M1;							
DT 01-MAY-1999 (TREMBLrel. 10, Created)							
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)							
DE Enamel matrix serine proteinase 1 precursor.							
GN KLK4.							
OS Mus musculus (Mouse).							
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.							
NCBI_TaxID=10090;							
RP SEQUENCE FROM N.A.							
RC STRAIN-SWISS-WEBSTER;							
RX MEDLINE=20152522; PubMed=10690663;							
RA Hu J.-C., Ryu O.-H., Chen J.-J., Uchida T., Wakida K., Murakami C., Jiang H., Qian Q., Zhang C., Ottmers V., Bartlett J.D., Simmer J.P.;							
RA "Localization of EMSP1 expression during tooth formation and cloning							

of mouse cDNA.";
 RT J. Dent. Res. 79:70-76(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 STRAIN-SWISS-WEBSTER;
 MEDLINE#-20323211; PubMed#-10863090;
 RX Hu J.C., Zhang C., Sun X., Yang Y., Cao X., Ryu O., Simmer J.P.;
 RA "Characterization of the mouse and human PRSS17 genes, their
 relationship to other serine proteases, and the expression of PRSS17
 in developing mouse incisors.";
 RR Gene 25:1-8(2000).
 :- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 TRYPsin FAMILY.
 CC EMBL: AF19894; AAC8894; 1.; -.
 DR MEROPS: S01_251; -.
 DR HSSP: P00763; 1DPO.
 DR MGI: MGI:1861379; Kika.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 SMART: SM00020; TRYPSIN_SP_C1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 SQ CHAIN 32 255 MATRIX SERINE PROTEINASE 1.
 SEQUENCE 255 AA; 27488 MW; 6FD2E7DEA0660A2A CRC64;

Query Match 52.2%; Score 72; DB 11; Length 255;
 Best Local Similarity 44.08%; Pred. No. 0.076;
 Matches 11; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Q9JIS2 PRELIMINARY; PRT; 255 AA.
 ID Q9JIS2
 AC Q9JIS2
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DR 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Enamel matrix serine proteinase 1 precursor.
 KLK4 Or PRSS17.
 Mus musculus (Mouse); Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Metazoa; Retheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10900.
 RN [1]
 RP SEQUENCE FROM N.A.
 STRAIN-129/SVJ;
 MEDLINE#-2023211; PubMed#-10863090;
 RX Hu J.C., Zhang C., Sun X., Yang Y., Cao X., Ryu O., Simmer J.P.;
 RA "Characterization of the mouse and human PRSS17 genes, their
 relationship to other serine proteases, and the expression of PRSS17
 in developing mouse incisors.";
 RR Gene 25:1-8(2000).
 :- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 TRYPsin FAMILY.
 CC EMBL: AF198931; AAC88937; 1.; -.
 DR HSSP: P00763; 1DPO.
 DR MEROPS: S01_251; -.
 DR MGI: MGI:1861379; Kika.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 SMART: SM00020; TRYPSIN_SP_C1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease.
 SQ SEQUENCE 270 AA; 6E5233084FBB13B7 CRC64;

Query Match 52.2%; Score 72; DB 5; Length 270;
 Best Local Similarity 60.0%; Pred. No. 0.008;
 Matches 12; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Q9BJL7 PRELIMINARY; PRT; 465 AA.
 ID Q9BJL7
 AC Q9BJL7
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DR 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Newborn larva-specific serine protease SS2.
 OS Trichinella spiralis.
 OC Eukaryota; Metazoa; Nematoda; Enoplia; Trichinella.
 OC Trichinellidae; Trichinella.
 DR NCBI_TaxID=6334; -.
 RN [1]

RESULT	12	Q967X8	PRELIMINARY;	PRT;	467 AA.
ID	Q967X8				
AC	Q967X8;				
DT	01-DEC-2001 (TREMBLrel. 19, Created)				
DT	01-JUN-2002 (TREMBLrel. 19, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DB	CUB-serine protease.				
OS	Panulirus argus (Spiny lobster).				
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;				
OC	Eumalacostraca; Eucaria; Decapoda; Pleocyemata; Palinura;				
OC	Palinuroidea; Pallinuridae; Panulirus.				
OX	NCBI_TAXID=6737;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Levine M.W., Walthall W.W., Tai P.C., Derby C.D.;				
RA	"Molecular cloning, characterization, cellular localization and				
RA	possible function of a CUB-serine protease in the olfactory system of				
RA	the spiny lobster <i>Panulirus argus</i> ."				
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL: AF372226; AAC48894.1;				
DR	InterPro: IPR000859; CUB-domain.				
DR	InterPro: IPR001254; Serine_protease_Try.				
DR	Pfam: PF00431; CUB; 1.				
DR	Pfam: PF00089; Trypsin; 1.				
DR	PROSITE: PS01180; CUB; 1.				
DR	PROSITE: PS50240; TRYPSIN_DOMAIN; 1.				
DR	PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.				
DR	PROSITE: PS00135; TRYPSIN_SER; UNKNOWN_1.				
KW	Hydrolase; Protease; Serine protease.				
SQ	SEQUENCE 467 AA; 50453 MW;				
Query	1 IVGGKEVTPHAYPWQVGLFTDDMY	50	0%	Score 69; DB 5;	Length 467;
Best Local Similarity	IVGGKEVTPEVNEYPWQVLLVTRDMY	58.3%		Fred. No. 0.039;	
Matches	14; Conservative	1		Mismatches 9;	Indels 0;
Qy					Gaps
Db					

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RESULT 13
09Y1V3 PRELIMINARY; PRT; 868 AA.
ID 09Y1V3; PRELIMINARY; PRT; 868 AA.
AC Q9Y1V3; PRELIMINARY; PRT; 868 AA.
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Tunicate retinoic acid-inducible modular protease precursor.
GN TRAMP
OS Polycarpa misakensis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
  Stolidobranchia; Styelidae; Polycarpa.
OX NCBI_TaxID:7723;
RN [1]
RP SEQUENCE FROM N.A.
RC TRAIN=WHITE SPOT;
RX MEDLINE=942646; PubMed=10491255;
RA Ohashi M., Kawamura K., Fujii N., Yubisui T., Fujiiwara S. ;
  RT "A retinoic acid-inducible modular protease in budding ascid
  Dev. Biol. 214:38-45 (1999).
RL 1 - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
  CC TRYPSIN FAMILY.
EMBL; AB030007; BAA82522.1; -
DR HSSP; P00763; 1DPO
  InterPro; IPR01311; Chymotrypsin.
  InterPro; IPR002172; Ldl_recept_A.
  InterPro; IPR003609; Pan_app.
  InterPro; IPR001254; Ser_protease_Try.
  InterPro; IPR001190; Srrcr_receptor.
  Pfam; PF00057; Ldl_recept_a_3.

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RX MEDLINE=99432219; PubMed=10500163;
 RA Lindsay L.L., Yang J.C., Hedrick J.L.;
 RT "Ovochymase, a Xenopus laevis egg extracellular protease, is
 translated as part of an unusual polyprotease",
 PROC. NATL. ACAD. SCI. U.S.A. 96:11253-11258(1999).
 [2]
 RN
 RP SEQUENCE FROM N.A.
 RA Yang J.C., Lindsay L.L., Hedrick J.L.;
 RT "cDNA Cloning of Ovochymase, a Chymotrypsin-like Protease Released
 From Xenopus laevis Eggs at Fertilization",
 Submitted (MAR 1996) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: CONTAINS 4 CUB DOMAINS.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 TRYPSIN FAMILY.
 DR EMBL: UB1290; AAC24717.1; -
 DR HSSP: P00763; 1DPO.
 DR MEROPS: S01.022; -
 DR MEROPS: S01.245; -
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000859; CUB_domain.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00431; CUB; 5.
 DR Pfam: PF00089; trypsin; 3.
 DR PRINTS: PR00722; CHYMTROPSIN.
 DR SMART: SM00042; CUB; 4.
 DR SMART: SM00020; TRYP_SPC; 3.
 DR PROSITE: PS01180; CUB; 5.
 DR PROSITE: PS50240; TRYPSIN_DOM; 3.
 DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_3.
 DR PROSITE: PS00135; TRYPSIN_SER; 3.
 DR Hydrolase: Serine protease.
 FT CHAIN 57 308 SERINE PROTEASE.
 FT CHAIN 584 817 SERINE PROTEASE.
 FT CHAIN 1295 1524 OVOCHYMASE.
 SQ SEQUENCE 1524 AA; 167566 MW; 32EFE42128F37268 CRC64;
 DR
 Query Match Score 69; DB 13; Length 1524;
 Best Local Similarity 57.9%; Pred. No. 0.13;
 Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 DR
 Query 1 IVGGXEVTPHAYPQVQGLF 19
 DR 11111:11111:1
 DR 584 IVGGEASPNSPWQVQIF 602
 DR
 RESULT 15
 O9PHQ6 PRELIMINARY; PRT; 263 AA.
 DR
 Query Match Score 69; DB 13; Length 1524;
 Best Local Similarity 57.9%; Pred. No. 0.13;
 Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 DR
 Query 1 IVGGXEVTPHAYPQVQGLF 19
 DR 11111:11111:1
 DR 584 IVGGEASPNSPWQVQIF 602
 DR
 SEQUENCE FROM N.A.
 RC TISSUE=PYLORIC CAECAL;
 RX MEDLINE=2046434; PubMed=11011764;
 RA Spiliarit R., Guadnadsdottir A.;
 RT "Molecular Cloning of the Atlantic Cod Chymotrypsinogen B",
 RL Microb. Comp. Genomics 5:41-50(2000).
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 TRYPSIN FAMILY.
 DR EMBL: AJ242521; CAB43766.1; -
 DR HSSP: P00766; 1CHG.
 DR MEROPS: S01.157; -
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser_protease_Try.